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Post-processing: Listing first 45 summaries
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Maximum DB seq length: 105
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Copyright (c) 1993 - 2000 Compugen Ltd.
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
Homo sapiens histone 1
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                                      gene, promoter region.
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M26162 Homo sapien
AF042300 Homo sapien
AF042301 Homo sapi
AF042302 Homo sapi
AF042302 Homo sapi
AF042302 Homo sapi
L30742 Human STS U
X55208 M.musculus
AU025275 Rattus no
I31337 Sequence 24
I31413 Sequence 32
X55226 M.musculus
AU046973 Rattus no
AF042305 Homo sapi
AF042308 Sequence 19
I31288 Sequence 19
I31288 Sequence 19
I31285 Sequence 20
I312949 Ovis aries
I31285 Sequence 19
I31307 Sequence 19
I3148 Sequence 20
I3148 Sequence 21
I31407 Sequence 23
I3141 Sequence 23
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I31319 Sequence 27
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  repeat_region
                                                                                                                                 3 (bases 1 to 73)
Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P. and Mignot,E.
Direct Submission
Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences,
Stanford University, Lab Surge Building, 1201 Welch Road, Rc
9126, Palo Alto, CA 94304, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 73)
Lin,L., Jin,L., Ximura,A., Carrington,M. and Mignot,E.
DO microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
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1 (bases 1 to 85)
Gallinari,P., La Bella,F. and Heintz,N.
Characterization and purification of HITF2, a novel CCAAT-binding protein that interacts with a histone H1 subtype-specific consens.
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Lin.L., Lin.X., Voros, A., Underhill, P. and Mignot, E. Microsatellite single nucleotide polymorphisms in the HLA-DQ Tissue Antigens 52 (1), 9-18 (1998)
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AF042300.1 GI:419
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/organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 75)
Lin,L., Jin,L., Kimura,A., Carrington,M. and Mignot,E.
DQ microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
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Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P.
Microsatellite single nucleotide polymorphisms
Tissue Antigens 52 (1), 9-18 (1998)
98378271
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                                                                                                                                                                                                                                                                                                1 Similarity 100.
                       AF042302 77 bp
Homo sapiens chromosome
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AF042302.1 GI:4191289
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Homo sapiens chromosome
AF042301
AF042301.1 GI:4191288
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/db_xref="taxon:9606"
/chromosome="6"
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tive 0; Mismatches
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40; Conserv
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Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences, Stanford University, Lab Surge Building, 1201 Welch Road, Room P126, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P. Microsatellite single nucleotide polymorphisms Tissue Antigens 52 (1), 9-18 (1998) 98378271
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I (bases 1 to 77)

Lin,L., Jin,L., Kimura,A., Carrington,M.,

DQ microsatellite association studies in

Notinens 50 (5), 507-520 (1997)
                                                  Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
primer A: GATCGAGAGCAGCCTGGA
primer B: TGGTGATTTGAAGGAATGCC
                                                                                                                                                                                Genetic and physical mapping of simple sequence sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 77)

1 (bases 1 to 77)

Gerken, S.C., Matsunami, N., Plaetke, R.; Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                          STS; PCR primer; STS sequence; microsatellite marker; sequence tagged site; tetranucleotide
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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three ethnic
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Rattus norvegicus,
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Cornall, R.J., Altman, T.J., Hearne, C.M. and Todd, J.A.
The generation of a library of PCR-analyzed microsatellite variants for genetic mapping of the mouse genome
Genomics 10 (4), 874-881 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-OCT-1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 97)
Hearne, C.M.
Direct Submission
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M.musculus D4nds1
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                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="NOD"
/db_xref="taxon:10090"
/chromosome="4"
/map="45 cM"
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       rvegicus, OTSUKA clone, sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus DNA, clone:0T48.13/788f08.
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The large-scale mapping of rat microsatellite markers unpublished (1998)
2 (bases 1 to 97)
Watanabe,T.K.
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                                                                                                                                                                                                                                                                               Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences method of using the same patent: US 5582979-A 249 10-DEC-1996;
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249 from patent
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//db_xref="taxon:10116"
//clone="Or48.13/788f08"
/note="Or48.13/788f08=-5'.-TCCAGTCCGTAGATTACATTTA-3',
/note="Or48.13/788f08x-5'-CGTGCATGCATTAGGC-3'"
Or48.13/788f08x-5'-CGTGCATGCATTAGGC-3'"
Or48.13/788f08x-3'
Or48.13/788f08x-5'-CGTGCATGCATTAGGC-3'"
                                                                                                                                                                                                              /organism="unknown"
21 c 0 g
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1. .97
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                                                                                                              0.1%; Score 38; DB 5; L
100.0%; Pred. No. 1.2e-07;
tive 0; Mismatches 0;
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100.0%; Pred. No. 3.5e-08;
Live 0; Mismatches 0;
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62 CACACACACACACACACACACACACACACACAA 25
                                                               Local Similarity
                       1 CACACACACACACACACACACACACACACACACAAA 38
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X55226
X5526.1 GI:50727
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131413

131413.1 GI:1822200
                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 87)
Cornall.R.J., Altman,T.J., Hearne,C.M. and Todd,J.A.
The generation of a library of PCR-analyzed microsatellite variants for genetic mapping of the mouse genome
Genomics 10 (4), 874-881 (1991)
                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same Patent: US 5582979-A 325 10-DEC-1996;
                                                                                                                                                                                                                        Submitted (22-OCT-1990) C.M. Hearne, UNIVERSITY OF OXFORD, NUFFI DEPT. SURGERY, LEVEL 6, JOHN RADCLIFFE HOSP., HEADINGTON OXFORD, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             microsatellite DNA. house mouse.
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24 c 0 q
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1. .51
                                                                                                                                              /note="D0nds8"
                                                                                                                                                                                                 organism-"Mus musculus"
                                                             0.1%; Score 38; DB 12;
100.0%; Pred. No. 1.1e-07;
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AFM249zg9;
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Gyapay,G., Morissette,J., Vignal,A., Dib,C., Fizames,C.,
Millasseau,P., Marc,S., Bernardi,G., Lathrop,M. and Weissenbach,J.
The 1993-94 Genethon human genetic linkage map
Nat. Genet. 7 (2 Spec No), 246-339 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-OCT-1992) Genethon, B.P. E-mail: Jean.Weissenbach@genethon.fr 2 (bases 1 to 100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; ver
Primates; Catarrhini; Hominidae;
1 (bases 1 to 100)
Shoeman,R.L.
Direct Submission
Submitted (23-JUN-1995) Shoeman R. L., Max-Planck-Institute fuer
Zellbiologie, Rosenhof, Ladenburg, Germany, D-68526
                                                                                            Wang,X., Tolstonog,G., Shoeman,R.L. and Traub,P
Selective binding of specific mouse genomic DNA
vimentin filaments in vitro
DNA Cell Biol. 15 (3), 209-225 (1996)
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 102)
                                                                                                                                                                                                                                                                 M.musculus
X89128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weissenbach, J., Gyapay, G., Dib, C., Vignal, A., Millasseau, P., Vaysseix, G. and Lathrop, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STS; CA repeat; dinucleotide repeat; GT repeat; microsatellite marker; repeat polymorphism.
                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A second-generation linkage map of the human Nature 359 (6398), 794-801 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/cell_line="CEPH 134702"
/clone_11b="genomic DNA"
a 31 c 10 g 24
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                                                                                                                                                                                                                                                              Submitted (11-DEC-1998) to the DDBJ/EMBL/GenBank databases. Takeshi K Watanabe, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima Tokushima (2014), Japan (E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe, T.K., Hishigaki, H., Okuno, S., Mizoguchi, A., Tsuji, A., Ono, T., Yamasaki, Y., Kanemoto, N., Takahash. Nakamura, Y., Takagi, Y. and Tanigami, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus, OT sequence tagged site.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Similarity
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                                                                                            /tissue_type="liver"
/note="109c04F=5'.CCCTTTCCTATTTTC-3',
109c04R=5'.AATTAAAGTATAAGGAAATACACAT-3'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_type=DIRECT
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/db_xref="taxon:10090"
                                                                                                                                                /cell_type="hepatocyte"
/clone="109c04"
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                                                                                                                                                                                                /organism="Rattus norvegicus"
/strain="Brown Norway"
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/rpt_unit=14. 15
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/function="sequence bound by
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Lin, L., Jin, L., Lin, X., Voros, A., Underhill, P. and Mignot, E. Direct Submission
Submitted (12-JN-1998) Psychiatry and Behavioral Sciences,
Stanford University, Lab Surge Building, 1201 Welch Road, Room
P126, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 69)
Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P. and Mignot,E.
Microsatellite single nucleotide polymorphisms in the HLA-DQ region
Tissue Antigems 52 (1), 9-18 (1998)
98378271
Homo sapiens
Eukaryota; Metakoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primatęs; Catarrhini; Hominidae; Homo.

1 (bases 1 to 83)
Lin, L., Jin, L., Kimura, A., Carrington, M. and Mignot, E.
DO microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
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DQ microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
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Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences,
Stanford University, Lab Surge Building, 1201 Welch Road, Room P126, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 83)
Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P. and Mignot,E.
Microsatellite single nucleotide polymorphisms in the HLA-DQ region
Tissue Antigens 52 (1), 9-18 (1998)
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larity 100.0%; Pred. No.
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/rpt_unit-ca
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RESULT 1 AF042305

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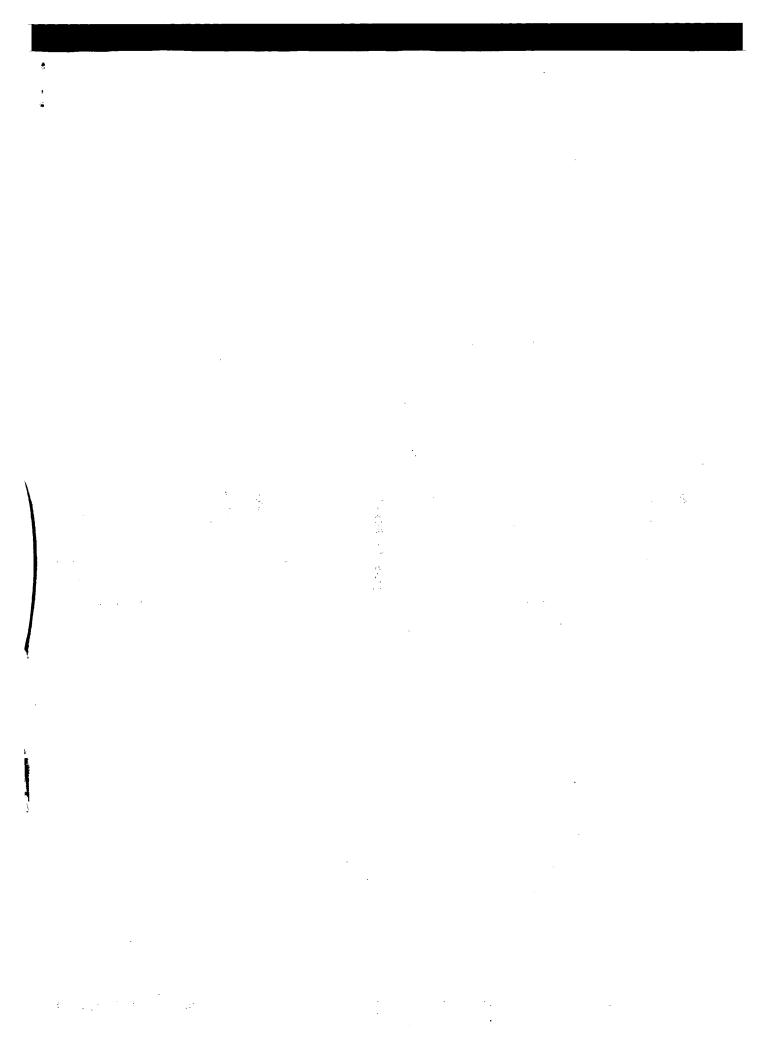
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Sequence 44 BP; 23 A; 21 C; 0 G; 0 U;
17-JUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd102.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
                                T65773 standard; DNA; 51 BP T65773;
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3 (3	commercial	ial ar	nimal or	plan	4	animal or plant breeding or pedigree analysis.	sis. Clones
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pr d(G-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

ps Claim 1; Column 13-14; 186pp; English.

Ps Claim 1; Column 13-14; 186pp; English.

CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC repeats, especially for use in e.g paternity or maternity testing,

CC human genetic analysis such as linkage analysis of genetic disease,

CC commercial animal or plant breeding or pedigree analysis. Clones

CC containing the repeat sequences were isolated by hybridisation of

CC chromosome-specific phage libraries with a synthetic poly(GC-dA).(dG-dT)

CC probe. Over 100 repeat blocks were isolated. The inserts from the clones

CC were amplified by primers T65798-T6607. Those clones where the repeat

CC sequence has been determined are shown in T65704-797. This repeat

CC sequence has been determined are shown in T65704-797. This repeat

CC sequence having the formula: (AC)19AA(AC)5A.

SO Sequence 51 BP; 27 A; 24 C; 0 G; 0 U;
gene mapping, and selective breeding
Table 7: Page 301: 517pp; English.
The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between
screening a library of bovine MboI DNA fragments of between
conclut of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and MboI sites, the frequency of
(76)n >9 microsatellites in the bovine genome is estimated at >100,
conclut of 50 clones cross-hybridised. Assuming independent
conclut of 50 clones cross-hybridised. Assuming independent
conclude the frequency of
the sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).
The sequences upstream and downstream of the microsatellite sequence
were used to generate the required PCR primers for in vitro
amplification of the corresp microsatellite (using the program
optification of the corresp microsatellite mapping of economic trait
coloci, or genes involved the determinism of economically important
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Best Local
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US558279-A.
10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
21-APR-1991; US-754351.
04-APR-1994; US-222177.
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15-JAN-1992; U00340.
15-JAN-1991; US-642342.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
GEORIGES M, Massey JM;
WPI; 92-284684/34.
Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FBB-1993 (first entry)
Microsatellite sequence from clone TGLA337.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus.
Bos taurus.
MO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q33930 standard; DNA; 60 BP.
Q33930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97-042299/04
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1 Similarity 100.0%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e analysis; genetic disease; isation; chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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0.00061
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10 033849/c
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AC 0338
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DE MICT
KW gene
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NOS-DS NOS-DS
PN W092
PD 06-A
PF 115-J
PR 115-J
PR 15-J
PR 15-
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Q33828/c
ID 20338
AC Q338
AC Q338
DT 02-F
DE M1CC;
KW PCR;
KW PCR;
KW Gene
OS Bos
PN WO92
PD 06-A
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PA (GERM) GENEVARY.

PA (GERM) GENEVARY.

DR WPI; 92-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding STAble 7; Page 269; 51/pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by cc screening a library of bovine mbor DNA fragments of between CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. CC one out of 50 clones cross-hybridised. Assuming independent CC (300 clones cross-hybridised. Assuming independent CC (301 clones cross-hybridised. Assuming independent CC (301 clones cross-hybridised. Assuming independent content of microsatellites and MboI sites, the frequency of (301 closs) partners in the bovine genome is estimated at >100, CC (301 closs) partners for ca. 230 such bovine microsatellites compared in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence complification of the corresp. microsatellite (using the program complification and in the general complification trait complication and in the general complification and interest complification and indexed herein (see below).

CC The sequence used to generate the required PC (using the program complification of the corresp. microsatellite (using the program complification of the corresp. microsatellite (using the program complification and indexed herein (see below).
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Best Local
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W09213102-A.

06-AUG-1992.

15-JAN-1992; U00340.

15-JAN-1991; US-642342.
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                                                                                       Q33828 standard; DNA; 36 BP.
Q33828;
Q25EB-1993 (first entry)
Microsatellite sequence from clone TGLA23.
PCR; selection; primers; OPTIRIM; breeding;
genetic mapping; traits; amplification; ss.
Bos taurus.
M09213102-A.
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Microsatellite sequence from clone TGLA26.
PCR; selection; primers; OPFIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                  06-AUG-1992.
15-JAN-1992; U00340
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37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 0.1%;
l Similarity 100.0%;
37; Conservative (
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Pred. No.
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Pred. No.
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0.0013;
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0.0013;
                                                                                                                                                                                                                        cattle;
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PS Table 7; Page 261; 517pp; English.

CC The sequence is that of a bowine microsatellite sequence obtd. by
CC screening a library of bowine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucjectide probe.
CC one out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bowine genome is estimated at >100,
CC (T6)n >9 microsatellites in the bowine genome is estimated at >100,
CC occ summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC traits esp. in cattle, to allow selective breeding.
CC see also Q33501-34437.
CC Sequence 36 BP; O A; O C; 18 G; 18 T;
               PA (GEMM-) GENMARK.

PA (GEMM-) GENMARK.

PR (GEMM-) GENMARK.

Recorded M. Massey JM:

PR (GEMM-) GENMARK.

PR (GEMM-) GENMARK
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Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA303. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
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(GENM-) GENMARK.
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15-JAN-1991; US-642342.
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0; Mismatches
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     18
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0.0031;
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Compared to the sequence is that of a bovine microsatellite sequence obtd. by the sequence is that of a bovine microsatellite sequence obtd. by the sequence is that of a bovine microsatellite sequence between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent of distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, occurred to the sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence upstream and downstream of the microsatellite sequence complification of the corresp. microsatellite (using the program of the total and the sequence of the microsatellite (using the program of the corresp. The sequence is to the sequence of the corresp. The sequence is to the sequence of the microsatellite (using the program of the corresp. The sequence is to the sequence of the sequence of the sequence of the corresp. The sequence of the sequence of the corresp. The sequence of the sequen
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Matches 36; Conser
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Best Local :
                                 W09213102-A.
06-AUG-1992; U00340.
15-JAN-1991; US-642342.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1993 (first entry)
02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA433.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for parentage testing, and in the genetic mapping of ecoloci, or genes involved the determinism of economically traits esp. in cattle, to allow selective breeding. See also 035501-34437.

Sequence 36 BP; 0 A; 0 C; 18 G; 18 T;
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WPI; 92-284684/34.
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15-JAN-1991; US-642342.
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Prable 7: Page 347: 517pp; English.
CC The sequence is that of a bowine microsatellite sequence obtd. by
CC screening a library of bowine MboI DNA fragments of between
CC 50 and 500 bp with an (AC)15 and a (CC)15 oligonucleotide probe.
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n > microsatellites in the bowine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bowine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC the sequences upstream and downstream of the microsatellite sequence
CC amplification of the corresp. microsatellite (using the program
CC opTIPRIM). The microsatellites microsatellite (using the program
CC opTIPRIM). The microsatellites and be used to identify individuals,
CC of arentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
See also 033501-34437.
See also 033501-34437.
See Sequence 37 BP; 0 A; 0 C; 18 G; 19 T;
                                                                                                                                                                                                                                                                                                               prigate mapping, and selective breeding
rable 7: Page 402; 517pp; English.

CC The sequence is a boyine microsatellite sequence obtd. by
cs screening a library of boyine Morrosatellite sequence so to be tween
cc 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC One out of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and Mbol Sites, the frequency of
cc (T6)n >9 microsatellites in the boyine genome is estimated at >100,
cc (00). The sequence information for ca. 230 such boyine microsatellites
cc is summarised in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence
cc amplification of the corresp. microsatellite (using the program
cc opTIPRIM). The microsatellites may be used to identify individuals,
cc for parentage testing, and in the genetic mapping of economic trait
cc loci, or genes involved the determinism of economically important
cc traits esp. in cattle, to allow selective breeding.
See also Q33501-34437.
See also Q33501-34437.
See also Q3501-34437.
                                                                                                                                   Query Match
Best Local Similarity
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Georges M, Massey JM;
WPI; 92-284684/34.
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Microsatellite sequence from clone TGLA94.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
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                                                                                     Conservative
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Pred. No. 0.0031
                                                                                                                                   Score 36; DB 1;
Pred. No. 0.0031
                                                                                     Mismatches
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                                                                                                                                                                                 Length 37;
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DB 1; 0.0031;

Length 37;

0

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Q33900/C

Q33900/C

AC Q33900

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AC Q33900

DT Q2-FBB

Micros

KW PCE; s

KW Genet!

MS B0513

PD 06-AUG

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PR 15-JAN

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PI GEORM-

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CC SEC 10C1,

CC SEC 11C1,

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PA (GENM-) GENNARK.

PA (GENM-) GENNARK.

DR WPI: 92-284684/34.

DR WPI: 92-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification, properly gene mapping, and selective breeding properly gene mapping, and selective broine microsatellite sequence obtd. by General State of Solones (AC)15 and a (TC)15 oligonucleotide probe. CC one out of 50 clones cross-hybridised. Assuming independent cdistribution of microsatellites and MboI sites, the frequency of (CC one out of 50 clones cross-hybridised. Assuming independent cdistribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program CC oppipriny). The microsatellites may be used to identify individuals, cf or parentage testing, and in the generatic mapping of economic trait crait craits esp. in cattle, to allow selective breeding.

See also (33501-34437.

See also (33501-34437.

See also (33501-34437.

See also (33501-34437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FBB-1993 (first entry)
Microsatellite sequence from clone TGLA310.
Microsatellite sequence from clone TGLA310.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus.
Bos taurus.
M09213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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Query Match 0.1%; Score 36; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 36; Conservative 0; Mismatches
w hybridisation; chromosome; ds.

Homo sapiens.

N US558297-A.

N US558297-A.

10 DEC-1996.

11 DEC-1996.

12 APR-1989; 341562.

R 05-SEP-1991; US-341562.

R 05-SEP-1991; US-754351.

R 04-ARR-1994; US-222177.

R (VARS-) MARSHFIELD CLINIC.

I Weber JI;

Weber JI;

Weber JI;

Weber JI;

Detection of polymorphic genetic markers of the form

Detection of polymorphic genetic markers as pri
                                                                                                                                                                                                                                                                                                                                                                                                                                   T65732 standard; DNA; 37 BP.
T65732;
T165732;
T17-TUN-1997 (first entry)
T17-TUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd30.
Repeat sequence; genetic marker; priner; amplification;
Polymorphism; repeat sequence; genetic marker; maternity; human; pedigree;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
Linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CACACACACACACACACACACACACACACACACACA
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Q

1 CACACACACACACACACACACACACACACACACACA 36

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Detection of polymorphic genetic markers of the form
pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
pr (dC-dA)n(dG-dT)n which can be used as genetic
proved the invention relates to the isolation of polymorphic repeat sequences
proved the invention relates to the isolation of polymorphic repeat of detect these
proved the invention of the sequence analysis of genetic disease,
proved the repeats which as linkage analysis of genetic disease,
proved the repeats which are alternating the termity of the repeats with no
proved interruptions and without adjacent repeats of another sequence;
proved the repeats which are defined as 2 or more runs of uninterrupted
proved the repeats which are uninterrupted runs of CA separated
proved the repeats which are uninterrupted runs of CA separated
proved the repeats which are uninterrupted mononucleotides; and
proved the repeats which are defined as for the perfect
compound repeats which are defined as for the perfect
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CC The invention relates to the isolation of polymorphic repeat sequences

CC having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC commercial for use in e.g paternity or maternity testing,

CC human genetic analysis such as linkage analysis of genetic disease,

CC commercial animal or plant breeding or pedigree analysis. Clones

CC containing the repeat sequences were isolated by hybridisation of

CC chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT)

CC probe. Over 100 repeat blooks were isolated. The inserts from the clones

CC were amplified by primers 765798-766047. Those clones where the repeat

CC sequence has been determined are shown in 765704-797. This repeat

CC sequence is from the marker clone Mdf30 which contains the repeat

CC sequence aving the formula (AC)185.

SQ Sequence 37 BP; 19 A; 18 C; 0 G; 0 U;
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Best Local s
Matches 36
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WPI; 97-042299/04.
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04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5582979-A.
10-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (dC-dA)n.(dG-dT)n polymorphic repeat sequence #1.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T66048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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36; Conser
                      e presented here (AC)19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341562.
; US-341562.
; US-754351.
; US-222177.
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                                               that the runs of CA
here is an example of
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Pred. No.
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0.0031;
<u>ن</u>
                                                  of.
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                                                  repeat sequence
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Query Match Best Local Similarity

0.1%;

Score 36; Pred. No

DB 1; 0.003;

Length

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PI Weber JJ;

DR WPI; 97-042299/04.

PT Detection of polymorphic genetic markers of the form

PT Detection of polymorphic genetic markers of the form

PT (dc-dA)n(dG-dT)n - using novel nucleic acid mols as primers

PS Disclosure; Column 11-12; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences

CC thaving the sequence (dC-dA)n.(dG-dT)n which can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC containing the sepecially for use in e.g paternity or maternity testing;

CC human genetic analysis such as linkage analysis of genetic disease,

CC containing the repeat sequences were isolated by hybridisation of

CC chromosome-specific phage libraries with a synthetic poly(dC-dA) (dG-dT)

CC probe. Over 100 repeat blocks were isolated. The inserts from the clones

CC were amplified by primers 765798-766047. Those clones where the repeat

CC sequence has been determined are shown in 765704-797. This repeat

CC sequence has been formula: (CA)19.

CS sequence avaing the formula: (CA)19.

CC sequence avaing the formula: (CA)19.

CC sequence avaing the formula: (CA)19.
RESULT 1
2336482
ID 0336
AC 0336
AC 02.F
DE Micri
KW PCR;
KW PCR;
KW 9092
PN W092
PN 15-J
PR 15-J
PR (GEN
DR WPI;
PT POly
PT gene
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T65750
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Matches 36
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21-APR-1989; 1
05-SEP-1991; 1
04-APR-1994; 1
Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding
                                 Georges M, Massey WPI; 92-284684/34.
                                                                                                                                                     Bos taurus
                                                                                                                                                                   Microsatellite sequence from clone MTGT4B. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                        Q33648 standard; DNA;
Q33648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T65750;
                                                                                                                     06-AUG-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1997 (first entry)

Repeat sequence from polymorphic marker clone Mfd50.

Repeat sequence from polymorphic marker; primer; amplification; Polymorphism; repeat sequence; genetic marker; primer; amplification; Polymorase chain reaction; paternity; maternity; human; pedigree; PCR; polymorase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T65750 standard;
                                                                                  15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                  (GENM-)
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                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                            0.1%;
l Similarity 100.0%
36; Conservative
                                                                  GENMARK.
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; US-341562.
; US-754351.
; US-222177.
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                                                                                                                                                                                                                      (first entry)
                                                   JK;
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0;
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Pred. No. 0.0
0; Mismatches
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0.003;
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                                                                                                                                                                                       cattle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 38
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Table 7; Page 189; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by creening a library of bovine mboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

Cone out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, clones from the sequence information for ca. 230 such bovine microsatellites on the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program of Themicrosatellites amplification of the corresp. microsatellite (using the program of corporately testing, and in the genetic mapping of economic trait traits esp. in cattle, to allow selective breeding.

See also 033501-34437.

Sequence 39 BP; 0 A; 0 C; 19 G; 20 T;

Query Match
Query Match
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 36; Conservative 0; Mismatches 0;

Length 39; Indels

0

Gaps

0

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RESULT 1
33807C
033807C
02380
AC 0238

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                                                                                                                                                                                                                                                                                                                                                                              PI Georges M, Massey JM;
PI Georges M, Massey JM;
PI Georges M, Massey JM;
PP Notyper S, Massey 
                                                                                                                                                       Query Match
Best Local Similarity
Matches 36; Conserv
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Microsatellite sequence from clone TGLA213.
Microsatellite sequence from clone TGLA213.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus
MO9213102-A.
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illarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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US-642342.
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39 CACACACACACACACACACACACACACACACACA

Search completed: March 29, 2000, 13:08:06 Job time: 33484 sec

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(without alignments)
-6778.337 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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RESULT 1
G31304
LOCUS
DEFINITION

ACCESSION

G31304 96 bp DNA STS 29-SEP-1998 \$y89991-19 Human (A.Gnirke) Homo sapiens STS genomic, sequence tagged site. G31304

ALIGNMENTS

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DEFINITION
ACCESSION
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AUTHORS
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Db 61 TCTGCCCCTTTCCCACTGTGCCCTGGGG 89
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Ouery Match
Dest Local Similarity 100.0%; Pred. No. 1.9e-34;
Matches 89; Conservative 0; Mismatches 0; Indels
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13127 56 bp DNA
Sequence 149 from patent US 5582979.
131237
131237.1 GI:1822028
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GDB_DSGG: D652377
Contact: Andreas Gnirke
Mercator Genetics, Inc.
4040 Campbell ave, Menlo Park CA, 94025, USA
Email: gnirke@mercator.com
Primer A: GTCCCCAAAGAATATAAATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 96)

Lauer, P., Meyer, N.C., Prass, C.E., Starnes, S.M., Wolff, R.K. and
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STS size: 77
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Genome Res. 7 (5), 457-470 (1997)
97294058
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Annealing:
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1 29 c 23 g
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/db_xref="taxon:9606"
/clone_lib="Human (A.Gnirke)"
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les 48; Conserv
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Homo sapiens DNA.

Homo sapiens DNA.

Homo sapiens DNA.

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota, Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 85)

1 (bases 1 to 85)

Characterization and purification of HITF2, a novel CCAAT-binding protein that interacts with a histone H1 subtype-specific consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMHISIPR 85 bp DNA PRI
Homo sapiens histone 1 gene, promoter region.
M26162
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                                                                                                                                                                                                                                                                                                      On Jul 23, 1994 this sequence version replaced gi:341438 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Mol. Cell. Biol. 9 (4), 1566-1575 (1989)
89261784
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1 (bases 1 to 56)
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                                                   0.2%; Score 46; DB 10; Length 85; ilarity 100.0%; Pred. No. 3.2e-12; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/cell_line="HeLa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Pred. No. 3e-13;
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                                                                                                                                 14 t
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AR002288

54 bp

DNA

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04-DEC-1998

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REFERENCE
AUTHORS
TITLE
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ORIGIN
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AR053139/c
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Matches 43
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TITLE
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                                                                                            HUMUT578A 69 bp
Human STS UT578, 5' pi
L39139 L18336
L39139.1 GI:642101
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Sequence 45
AR053139
AR053139.1
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AR002288
                                                                                                                                                                                                                                       ch 0.2%; Score 43; DB similarity 100.0%; Pred. No. 1: 43; Conservative 0; Mismatches
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Orr,H.T., Ranum,L.P.W., Chung,M. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1 and method
                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 54)
Orr,H.T., Ranum,L.P.W., Chung,M. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1
                                              Homo sapiens
                                                                  STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                                                                                                                                Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
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Gerken, S.C., Matsunami, N., Plaetke, R.,
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 69)
                                                            Homo sapiens DNA.
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Location/Qualifiers
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45 from pat
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26 c 0 g
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26 c 0 g
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J. 1.1e-10;
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1.1e-10;
hes 0; Indels
Albertsen, H.,
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Ballard, L.
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Matches 40
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             TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
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Sequence 1 from
A68621
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                                                          0.2%;
llarity 100.0%;
Conservative (
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10109 TTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAA 10150
8640 TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
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Submitted by: Utah Center for Human Genome Research Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
primer A: AGTTCGAGACCAGCCTGGC
primer B: AGGTGCGAGAAAATCGCATC
                                                                                                                                                                                                                                                                                        1 (bases 1 to 40)

Resnick,M.A., Larionov,V.L., Kouprina,N.Y. and Perkins,E.L.

TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING

Patent: WO 9801573-A 15-JAN-1998;

US HEALTH (US)
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Cycles Denaturation Annealing
C 10 sec. 62 C 10 sec. 72 C 20 sec. 158 C 10 sec. 72 C 20 sec. Mg++: 1.50 r
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
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Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and
White,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19"
14..32
                                                                                                                                                                                    /db_xref="taxon:32644"
12 c 13 g
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/evidence=experimental
16 c 14 g 1
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n Patent WO9801573.
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; Pred. No. 3.7e-10;
0; Mismatches 0;
                                                                               Score 40; DB 5; L
Pred. No. 4.1e-09;
                                                             Mismatches
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                                                                                                   Length 40;
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LOCUS DEFINITION ACCESSION

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AUTHORS

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REMARK

SOURCE ORGANISM

Homo sapiens

KEYWORDS

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Ouery Match 0.2%; Score 40; DB 10; Length 101; Best Local Similarity 100.0%; Pred. No. 4e-09; Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        $79561 101 bp DNA GHER (PRI ) PRI GHER (PATTIAN-1996 GHRX (PARTIAL GENOMIC GUPLICATION STATEPOINT) (human, acute myeloid leukemia with trisomy 11 syndrome patient J, Genomic Mutant, 101
                                                                                                                                        GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 170936] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Bernard,O.A., Romana,S.P., Schichman,S.A., Mauchauffe,M.,
Jonveaux,P. and Berger,R.

Partial duplication of Hrx in acute leukemia with trisomy il

Leukemia 9 (9), 1487-1490 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenBank staff at the National Library of Medicine created this entry [NCBI gibbsg 170933] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Bernard,O.A., Romana,S.P., Schichman,S.A., Mauchauffe,M.,
Jonveaux,P. and Berger,R.
Partial duplication of HRX in acute leukemia with trisomy 11
Leukemia 9 (9), 1487-1490 (1995)

95387660
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HRX (Intron 6) [human, Genomic, 101 nt].
$79560
$79560.1 GI:1168041
                                                                                                     Authors indicate breakpoint region at 48-62 
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                     human acute myeloid leukemia with trisomy 11 syndrome patient
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21 c
/partial
/gene="dHRX"
                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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FEATURES
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182155/c
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I31174/c
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ORGANISM
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Best Local S
Matches 40
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Best Local S
Matches 39
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Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                               TITLE
16299 CCTGGGTGCTCCACCTGGCACGTATATCTCTGCTCTTCC 16337
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Sequence 86 from patent US:
131174
131174.1 GI:1821065
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1 from patent US
182155
                                                                                                                                                                                                                                                                                1 (bases 1 to 39)
Tsuchihashi,Z., Gnirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D.,
Wolff,R.K. and Feder,J.N.
                                                                                                                                                                                                           Patent: US 5712098-A 1 27-JAN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                               Hereditary hemochromatosis diagnostic markers and diagnostic
                                                                                                                                                                                                                                                                                                                                    Unclassified
                                                                                                                                                                                                                                                                                                                                                                       Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                         I82155.1 GI:3210452
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method of using the same
Patent: US 5582979 A 86 10-DEC-1996;
Location/Qualifiers
1. .39
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ilarity 100.0%; Pred. No. 1.3e-08;
Conservative 0; Mismatches 0;
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                                                    0.2%; Score 39; DB 5; L llarity 100.0%; Pred. No. 1.3e-08; Conservative 0; Mismatches 0;
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8 c 15 g
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18 c 0 g
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RESULT 9 S79561 LOCUS DEFINITION

SOURCE ORGANISM

Homo sapiens

KEYWORDS ACCESSION VERSION

REFERENCE

AUTHORS

JOURNAL MEDLINE REMARK

TITLE

BASE COUNT ORIGIN

gene

FEATURES

COMMENT FEATURES

source

gene

Gaps

0

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REFERENCE
AUTHORS
TITLE
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                                                                       Ovis aries DNA.

Ovis aries

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi

Caprinae; Ovis.

1 (bases 1 to 102)

Crawford, A.M. and Buchanan, F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF042304
Homo sapiens
AF042304
                                                                                                                                                                                                Sheep dinucleotide repeat polymorphism at
                                                 Ovine dinucleotide repeat polymorphisms FCB193, FCB266 and FCB304 loci
                                                                                                                                                            dinucleotide repeat polymorphism
                                                                                                                                                                           L01534.1 GI:165865
                                                                                                                                                                                        L01534
                                       Unpublished (1992)
                                                                                                                                                                                                                SHPDINUCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences, Stanford University, Lab Surge Building, 1201 Welch Road, Room P126, Palo Alto, CA 94304, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 75)
Lin,L., Jin,L., Kimura,A., Carrington,M. and Mignot,E.
DQ microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin,L., Jin,L., L:
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P. Microsatellite single nucleotide polymorphisms Tissue Antigens 52 (1), 9-18 (1998) 98378271
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/organism="Ovis aries'
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/db_xref="taxon:9606"
/chromosome="6"
                          Location/Qualifiers
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FCB266 locus.
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Sequence
AR002290
 1 Similarity 100 38; Conservative
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AR051487
                                                                                                                                            1 (bases 1 to 66)
Orr.H.T., Ranum,L.P.W., Chung,M. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 60)
de la Monte, S. and Wands, J.R.
Meural thread protein gene expression
                                                                                                                         Patent:
                                                                                                                                                                                                 Unknown
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/cell_type="leukocyte"
31. .69
                                                                       /organism="unknown"
0 c 31 g
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14 c 15 g
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tive 0; Mismatches 0;
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Page 6

Search completed: March 29, 2000, 17:18:26 Job time: 50055 sec

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STS genomic, sequence
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G31304 sy899g1-19
AF062763 Glycine m
G37948 C44M78 Plasm
G37948 C44M8 Plasm
G37948 C4MM8 Plasm
M15365 Human low d
L36843 Homo sapien
M15365 Human low d
AF062763 Glycine m
M87899 Human carci
I82155 Sequence 1
I88893 Sequence 1
I88893 Sequence 1
M36131 Human alpha
A66622 Sequence 2
AR063068 Sequence 2
AR063068 Sequence 3
AR063068 Sequence 3
AR063068 Sequence 1
A49118 Sequence 13
A49118 Sequence 13

Description

AR001312 Sequence

K03555 Human low d
129931 Sequence 4

A48799 Sequence 6
136502 Sequence 1
18994 Sequence 7
18994 Sequence 8
16 S76510 D1S8 (B) (h
16 S76510 D1S8 (B) (h
17 S76510 D1S8 (B) (h
18 S76510 D1S8 (B
18 S76510 D1S

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Best Local :
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                                                                                                           931 TCTGCCCCTCTTCCCACTGTGCCCTGGGG 959
                                                                                                                                                                              871 CTGCTGGTGTCCCCAAAGAATATAAAATGAGAAAAATGCTTCCCATGGATGCCAGATCCCC 930
                                                                                                                                                                1 CTGCTGGTGTCCCCAAAGAATATAAATGAGAAAAATGCTTCCCATGGATGCCAGATCCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Andreas Gnirke
Mercator Genetics, Inc.
4040 Campbell Ave, Menlo Park CA, 94
Email: gnirke@mercator.com
Primer B: AGGCANAGANTATAAATGAG
Primer B: AGGCACAGTGGGAAG
STS Size: 77
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G31304.1
STS.
AF062763 92 bp DNA
Glycine max microsatellite
AF062763
AF062763.1 GI:3372757
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GDB_DSEG: D6S237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone-contig and STS maps of the hereditary hemochromatosis region on human chromosome 6p21.3-6p22 Genome Res. 7 (5), 457-470 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lauer,P., Meyer,N.C., Prass,C.E., Starnes,S.M., Wolff,R.K. and Gnirke,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PCR Cycles:
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Annealing:
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Total Vol:
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29 c 23 g
                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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-HCl: 10 mM
8.3
-Lin: 0.001% (W/V).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 each 0.8 um
each 200 um
: 0.05 units/ul
12 ul
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60 degrees C for 45 s
72 degrees C for 60 s
35
MJ Research PTC-200
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                          AC21 repeat region.
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for 60 seconds
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                                                                                                       Bldg. 4, Room 126, NIH Campus, 1
Tel: (301) 496-4021
Fax: (301) 402-0079
Email: tew@helix.nih.gov
Primer B: GARATMIATCACAGAGCAATC
Primer B: AATTTACTTCCTGCATTTTCC
                                                                                                                                                                                                       Contact: Thomas E. Wellems LPD
                                                                                                                                                                                                                                                                                                                                                                   G37948.2 GI:4337425
            Protocol:
                            Machine:
                                                     Initial heat:
Cycles:
                                                                                STS size: 99
PCR Profile:
                                                                                                                                                                                                                                                                                                                                         malaria parasite P. falciparum.
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Peakall, R., Gilmor
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/db_xref="taxon:3847"
6. .57
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Peakall, R., Gilmore, S., Keys, W., Morgante, M. and Rafalski, A. Cross-species amplification of soybean (Glycine max) simple-sequence-repeats (SSRs) within the genus and other legume genera: implications for the transferability of SSRs in plants 2 (bases 1 to 92) In press 2 (bases 1 to 92) Peakall, R., Gilmore, S., Keys, W., Morgante, M. and Rafalski, A. Direct Submission Submitted (04-MAY-1998) Division of Botany and Zoology, Australian National University, Canberra, ACT 0200, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           soybean.
Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 99) Su,X-z., Ferdig,M.T. and Wellems,T.E. Integrated genetic and physical maps of Plasmodium falciparum Unpublished (1998) On Mar 6, 1999 this sequence version replaced gi:3056692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G37948 99 bp DNA STS 26-FEB-1999 C4M78 Plasmodium falciparum haploid Plasmodium falciparum STS genomic, sequence tagged site.
G37948 G37948
2min at 94oC
30 cycles, each having steps 20sec at 94oC;
10sec at 45oC; 10sec at 40oC; 30sec at 60oC
Perkin Elmer GeneAmp 9600
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G37948
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Integrated genetic and physical maps of Plasmodium falciparum
Unpublished (1998)
On Mar 6, 1999 this sequence version replaced q1:3056692.
                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 99)
                                                                                                                                                                     Tel: (301) 496-4021
Fax: (301) 402-0079
Email: tewGhelix nih.gov
Primer A: GGAANTATACACAAGCAATC
Primer B: AATTTACTTCCTGCATTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   G37948.2 GI:4337425
                                                                                                                                                                                                                                                                                        Contact: Thomas E. Wellems
                                                                                                                                                                                                                                                                                                                                                                                                                     malaria parasite P. falciparum
                                                                        Protocol:
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6 c 10 g
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/dev_stage="erythrocytic haploid stage"
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/strain="HB3xDd2"
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30 cycles, each having steps 20sec at 94oC;
10sec at 45oC; 10sec at 40oC; 30sec at 60oC
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5 pM each
0.3 ul of :
0.5 unit
15 ul
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0.3 ul of 10 mM stock solution
0.5 unit
15 ul
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l Similarity 100.0%;
44; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                               Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987). Individual FH 295 carries two mutant LDL receptor alleles. The allele below was inherited from the father and includes a duplication of exons 2 through 8 that was presumably created by unequal chromosomal crossover involving Alu repeats in introns 1 and 8. The exact site of recombination cannot be determined because the sequences of the Alu repeats in introns 1 and 8 of normal alleles are identical over a span of 26 nucleotides at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90)
1 (bases 1 to 90)
1 (chanan, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alu-Alu
recombination in a subject with familial hypercholesterolemia
Cell 48 (5), 827-835 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M15365.1 GI
Alu repeat;
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    upstream
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1.5 mm MgCl2
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/dev_stage="erythrocytic haploid stage"
1. .99
1. .20
                                                                                                                                                                                                      /gene="LDLR"
<1. .43
//note-"LDLR duplicated intron 1 (no splice of 68); putitive; does not fit consensus" 3 c 19 g 20 t cream of NheI site; chromosome 19p13.2-p13.1.
                                                                                            /organism="Homo sapiens" 68. .>90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(79. .99)
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                                                                                                                                                      /note="LDLR intron 8; G00-119-362"
                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                 'gene="LDLR"
                                                                                                                                                                                                                                                                    /map="19p13.3"
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                                                                                                                                        . 68
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D. 1.7e-11;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                        d2; Conserv
Clean copy of sequence kindly provided by M.Lehrman (22-APR-198: Individual FH 295 carries two mutant LDL receptor alleles. The allele below was inherited from the father and includes a duplication of exons 2 through 8 that was presumably created by
                                                                                                                                                                                                                                                                        HUMLDLRM 90 bp DNA PRI Human low density lipoprotein receptor mutant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 89184542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMALUANCD
Homo sapie
                                                                    1 (bases 1 to 90)
Lehrman,M.A., Goldstein,J.L., Russell,D.W. and Brown,M.S.
Lehrman, of the seven exons in LDL receptor gene caused by Alu-Alu
recombination in a subject with familial hypercholesterolemia
Cell 48 (5), 827-835 (1987)
                                                                                                                                                                        recombination.
Human (FH 295) fibroblast DNA, clone p295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                 Alu repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ancient DNA: extraction, characterization, molecular cloning, enzymatic amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment 12:5.
L36843
                                                                                                                                                                                                                                M15365.1 GI:187107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (individual_isolate 4000 year old remains from Nekht-ankh) liver DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alu repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L36843.1 GI:556196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
18 c 23 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Homo sapiens"
/isolate-"4000 year old |
/db_xref-"taxon:9606"
/tissue_type-"liver"
<1. .>67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                 LDL receptor; cell surface protein; crossover;
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Pred. No. 5.6e-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               remains from Nekht-ankh"
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1 Alu repeat
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                                                                                                                                                                                                                                                                            recombination
                                         (22-APR-1987).
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AF062763/c
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             Query Match 0.1%; Strest Local Similarity 100.0%; 1 Matches 41; Conservative 0;
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Glycine max
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Score 41; DB; Pred. No. 6.:
0; Mismatches

DB 8; Le.. J. 6.3e-10; O;

Length 92;

Indels

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Oy 23593 GTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGG 23633
Db 78 GTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGG 38
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                                                                                                                                                                                                                                                     Direct Submission
Submitted (04-MAY-1998) Division of Botany and Zoology, Australian National University, Camberra, ACT 0200, Australia
                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 92)

PeakAll,R., Gilmore,S., Keys,W., Morgante,M. and Rafalski,A.

PeakAll,R., Gilmore,S., Keys,W., Morgante,M. and Rafalski,A.

Cross-species amplification of soybean (Glycine max)

Simple-sequence-repeats (SSRs) within the genus and other legume genera: implications for the transferability of SSRs in plants Mol. Biol. Evol. (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ervou/oj 92 bp DNA
Glycine max microsatellite AC21 repeat
AF062763
                                                                                                                                                                                                                                                                                                                                 Mol. Biol. Evol. (1998) In press
2 (bases 1 to 92)
Peakall_R., Gilmore,S., Keys,W., Morgante,M. and Rafalski,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytas; Spermatophyta; Magnollophyta; eudicotyledoma; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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18 a 33 c 19 g 20 t
upstream of NheI site; chromosome 19p13.2-p13.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.1%; Score 41; DB 9; L larity 100.0%; Pred. No. 6.3e-10; Conservative 0; Mismatches 0;
                                                                                                             /organism="Glycine max"
/db_xref="taxon:3847"
6. .57
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/rpt_type=tandem
/rpt_unit=ta
5 c 4
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/db_xref="taxon:9606"
/map="19p13.3"
                                                                                      /note="microsatellite AC21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="LDLR intron 8; G00-119-362"
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HUMALCE272/c
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                                                             Query Match 0.1%; Score 39; Best Local Similarity 100.0%; Pred. No. Matches 39; Conservative 0; Mismatc
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            39
         182155 39 bp
Sequence 1 from paten
182155
182155.1 GI:3210452
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1 (bases 1 to 104)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens male embryo carcinoma cDNA to other RNA Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human carcinoma
M87899
                                                                                                                                                                      Patent: US 5712098-A 1 27-JAN-1998;
Location/Qualifiers
1. .39
                                                                                                                                                                                                                                      1 (bases 1 to 39)
Tsuchihashi, Z., Gnirke,
Wolff, R.K. and Feder, J
                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M87899.1 GI:174875
                                                                                                                                                                                                                        Hereditary hemochromatosis diagnostic markers and diagnostic
                                                                                                                                                                                                                                                                                                         Unknown.
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                                                                                                                                                                                                                                                                              Unclassified.
                                                                                                                                          /organism~"unknown"
8 c 15 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="carcinoma"
26 c 37 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'sex="male"
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na cell-derived Alu RNA transcript,
                                                                                                                                                                                                                                                                                                                                                         39 bp
m patent
                                                                                                                                                                                                                                                   Gnirke, A., Thomas, W.J., Drayna, D.T., Ruddy, D.,
                                                                                                                                                                                                                                                                                                                                                            DNA
US 5712098
                                                              Mismatches
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                                                                                                      22
                                                                                                     GCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCAC
           A68622 40 bp DNA
Sequence 2 from Patent WO9801573.
A68622
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Sequence 11 from patent US
188893
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J. Biol. Chem. 265, 9319-9326 (1990)
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нимвиккгаа 80 bp DNA
Human alpha-galactosidase breakpoint region
M36131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fabry disease; breakpoint junction; glycosphingolipid catabolism \operatorname{Human\ DNA}.
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Suzuki,F., Hiraki,Y., Takahashi,K., Suzuki,J., Kondo,J., Kohara,A.,
Mori,A. and Yamada,E.
Human chondromodulin-I protein
Patent: US 5719125-A 11 17-FEB-1998;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 Similarity 100.0%; Pred. No. 2.4e-08;
38; Conservative 0; Mismatches 0;
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1 (bases 1 to 40)

1 (bases 1 to 40)

Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and Perkins, E.L.

TRANSFORMATION ASSOCIATED RECOMBINATION CLONING

Patent: WO 9801573-A 15-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unidentified
unidentified
Homo sepiens
Homo sepiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 62)
1 (bases 1 to 62)
Fleming/J.C., Pahl/H.L., Gonzalez,D.A., Smith/T.F. and Tenen,D.G.
Structural analysis of the CD11b gene and phylogenetic analysis of
                                                                                                                                                   $52152531 62 bp DNA PRI 08-MAY-1993 CD11b-leukocyte integrin alpha chain [human, Genomic, 62 nt, segment 31 of 31] $52228 $5228 GI:263048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: US 5844075-A 42 01-DEC-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.

1 (bases 1 to 58)

1 (kawakami,Y. and Rosenberg,S.A.

Melanoma antigens and their use in diagnostic and therapeutic
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Sequence 42 from patent US 5844075.
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Map location: 16.
                                                                                                                                                                                                                                                                                                                              the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during
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J. Immunol. 150 (2), 480-490 (1993)
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Search completed: March 30, 2000, 00:22:34
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-222-177A-119
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Seguence	Sequence	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
134, Ap	116, Ap	550611	244, Ap	382, Api	128, App	394, Apı	307, App	65, App.	304, Ap	391, App	337, App	317, App	89, App	•	•	•	•
	36 0.1 65 1 US-08-222-177A-134 Sequence	36 0.1 65 1 US-08-222-177A-116 Sequence : 36 0.1 65 1 US-08-222-177A-134 Sequence :	42 36 0.1 62 7 5506118-3 43 36 0.1 65 1 US-08-222-177A-116 Sequence 43 36 0.1 65 1 US-08-222-177A-134 Sequence	41 36 0.1 60 1 US-08-222-177A-244 Sequence: 42 36 0.1 62 7 5506118-3 43 36 0.1 65 1 US-08-222-177A-116 Sequence: 44 36 0.1 65 1 US-08-222-177A-134 Sequence:	40 36 0.1 57 1 US-08-222-177A-382 Sequence 41 36 0.1 60 1 US-08-222-177A-244 Sequence 42 36 0.1 62 7 5506118-3 Patent No. 43 36 0.1 65 1 US-08-222-177A-116 Sequence 43 36 0.1 65 1 US-08-222-177A-134 Sequence 44 36 0.1 65 1 US-08-222-177A-134 Sequence	39 36 0.1 57 1 US-08-222-177A-128 Sequence 40 36 0.1 57 1 US-08-222-177A-382 Sequence 41 36 0.1 60 1 US-08-222-177A-244 Sequence 42 36 0.1 62 7 5506118-3 Patent No. 42 36 0.1 65 1 US-08-222-177A-116 Sequence 43 36 0.1 65 1 US-08-222-177A-134 Sequence	38 36 0.1 56 1 US-08-222-177A-394 Sequence 39 36 0.1 57 1 US-08-222-177A-128 Sequence 40 36 0.1 57 1 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Sequence	33 36 0.1 51 1 US-08-222-177A-337 Sequence 35 36 0.1 51 1 US-08-222-177A-391 Sequence 35 36 0.1 53 1 US-08-222-177A-304 Sequence 36 0.1 56 1 US-08-222-177A-65 Sequence 37 36 0.1 56 1 US-08-222-177A-307 Sequence 38 36 0.1 56 1 US-08-222-177A-394 Sequence 39 36 0.1 57 1 US-08-222-177A-128 Sequence 40 36 0.1 57 1 US-08-222-177A-382 Sequence 41 36 0.1 60 1 US-08-222-177A-244 Sequence 42 36 0.1 65 1 US-08-222-177A-116 Sequence 43 36 0.1 65 1 US-08-222-177A-116 Sequence 44 36 0.1 65 1 US-08-222-177A-134 Sequence	32 36 0.1 51 1 US-08-222-177A-317 Sequence 33 36 0.1 51 1 US-08-222-177A-337 Sequence 34 36 0.1 51 1 US-08-222-177A-337 Sequence 35 36 0.1 51 1 US-08-222-177A-304 Sequence 36 0.1 53 1 US-08-222-177A-304 Sequence 37 36 0.1 56 1 US-08-222-177A-307 Sequence 38 36 0.1 56 1 US-08-222-177A-307 Sequence 39 36 0.1 56 1 US-08-222-177A-394 Sequence 39 36 0.1 57 1 US-08-222-177A-128 Sequence 40 36 0.1 57 1 US-08-222-177A-382 Sequence 41 36 0.1 57 1 US-08-222-177A-384 Sequence 42 36 0.1 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ALIGNMENTS

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Sequence 249, Application US/08222177A Patent No. 5582979
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
EILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
NUMBER OF SEQUENCES: 460
                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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IMMEDIATE SOURCE: CLONE: mfd69rs
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                                                                                                                                                                                               TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                            nucleic acid
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RESULT 2
US-08-222-177A-325
; Sequence 325, App
US-08-222-177A-140
US-08-222-177A-140
Sequence 140, Application US/08222177A
Patent NO. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME;
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
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US-08-222-177A-325
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GENERAL INFORMATION:
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Best Local S
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TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dewistre STREET: 8000 Ex CITY: Madison STATE: Wisconsi
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Local Similarity 100.0%; Pred. No. 0.00016;
hes 38; Conservative 0; Mismatches 0;
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8000 Excelsior Drive, Suite 401
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US-08-222-177A-198
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PATENT NO. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING
NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:
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Best Local S
Matches 36
                     ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                            ADDRESSEE: DeWitt Ross & Stevens, S.C. STREET: 8000 Excelsior Drive, Suite 401 CITY: Madison STATE: Wisconsin COUNTRY: USA ZIP: 53717-1914
        FILING DATE:
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Conservative

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MOLECULE TYPE: DI
; IMMEDIATE SOURCE:
; CLONE: mfd30rs
US-08-222-177A-140
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SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
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PRIOR APPLICATION DATA:
APPLICATION UNMER: US 07/341
APPLICATION UNMER: US 07/341
APPLICATION UNMER: US 07/341
APPLICATION UNMER: US 07/341
NAME: Sara, Charles S.
NAME: Sara, Charles S.
RESERSINCE/DOCKET UNMER: 0986
TELECOMMUNICATION INFORMATION:
TELEPINONE: (608) 831-2100
TELEPINE: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/222,177A
APPLICATION NUMBER: US/08/222,177A
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DeWitt
STREET: 8000 Exce
CITY: Madison
STATE: Wisconsin
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ZIP: 53717-1914
  Local Similarity
les 36; Conserv
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                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                       double
0.1%; Score 36; DB 1; L
100.0%; Pred. No. 0.00085;
ative 0; Mismatches 0;
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                                             Length 37;
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CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/
APPLICATION NUMBER: 21-APR-1989

07/341,562

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US-08-222-177A-198
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 397, Application US/08222177A Patent No. 5582979
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Best Local :
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                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: SAIRA, Charles S.
REGISTRATION NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0988
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATER: PC POOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Weber, James L.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: GRADISON THY: Madison
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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36; Conservative C
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wisconsin
                                                                                   (808)
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Pred. No.
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RESULT

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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
US-08-222-177A-397
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                                                                                                                                     US-08-222-177A-137
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                                                            Matches
                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                   IMMEDIATE SOURCE: CLONE: mfd29rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                            1 CACACACACACACACACACACACACACACACACA 36
 2 CACACACACACACACACACACACACACACACACA 37
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36; Conserv
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                                                                                                                                                                                                                           nucleic acid
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8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                         : (608) 831-2100
(608) 831-2106
                                                            Conservative
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                                                                                                                                                                                                                double
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                                                                            100.0%;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                  30,492
                                                                                                                                                                                                                                                                            137:
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                                                                            Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                       09865.601
                                                            Mismatches
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                                                                            DB 1; L
. 0.00084;
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                                                            Gaps
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US-08-222-177A-119
; Sequence 119, Application US/08222177A
; Patent No. 5582979
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US-08-222-177A-400
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                                                                                                           Sequence 400, Application US/U8ZZZI//A

Sequence 400, Application US/U8ZZZI//A

Patent NO. 5582579

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION NUMBER: US/08/222,177A
FILING DATE: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTONNEY/AGENT INFORMATION:
NAME: SATA, ChATLES S.
REGISTRATION NUMBER: 09865.601
TELEPENONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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APPLICANT: Weber, James L.

APPLICANT: Weber, James L.

TITLE OF INVENTION: (LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:

ADDRESSPER: DeWitt Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401

CITY: Madison

STATE: Wisconsin

COUNTRY: USA

ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 119: SEQUENCE CHARACTERISTICS:
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CLONE: mfd23rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
COMPUTER READABLE FORM:
                                                        STREET: 8000 Exce
CITY: Madison
STATE: Wisconsin
                       COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.1%; Score 36; DB 1; L
Local Similarity 100.0%; Pred. No. 0.00084;
les 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READRAIL FORM:

COMPUTER READRAIL FORM:

COMPUTER: IDM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/222,177A

FILING DATE: 435

PRIOR APPLICATION UNMBER: US 07/341,562

FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,492

REFERENCE/DOCKET NUMBER: 09865.601

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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US-08-222-177A-403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Query Match
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDATE: Madison
STATE: Wisconsin
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DeWitt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (608) 831-2106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08222177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/222,177A
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

403:

LENGTH:

40 base pairs

nucleic acid

double

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                                                                                                          US-08-222-177A-74
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Patent No. 5582979
GENERAL INFORMATION:
                        Query Match
Best Local Similarity
Matches 36; Conserv
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Best Local
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341
FILING DATE: 21 APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                       MOLECULE TYPE: D
IMMEDIATE SOURCE:
CLONE: mfd8rs
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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1 CACACACACACACACACACACACACACACACA 36
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                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                              (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weber, James L.
                                Conservative
                                                                                                                                                                    linear
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                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                    double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH POLYMORPHISMS IN (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.1%; Score 36;
100.0%; Pred. No.
                                           0.1%; Score 36;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                      US 07/341,562
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No. 0.00084;
0;
                                             DB 1; I
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                                                           Length 41;
                              Indels
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                              0
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                              Gaps
                              0,
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IMMEDIATE SOURCE:
; CLONE: mfd45rs
US-08-222-177A-183
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                                                                                                                                                                   US-08-222-177A-232
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                                                                                                                               Sequence 232, Application US/08222177A Patent No. 5582979
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
                                              GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUEN
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Weber, James TITLE OF INVENTION: LENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sara, Charles S. REGISTRATION NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Madison
                                                                                                                                                                                                                                   Local Similarity
es 36; Conserv
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82979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
E: DeWitt Ross & Stevens, S. 8000 Excelsior Drive, Suite
                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
                                                                                                                                                                                                                                                                                                                0.1%; Score 36;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ames L.

(dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/341,562
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                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                   SEQUENCES
                                                                                                                                                                                                                                                                                                                    0.00083;
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                                                                   AND METHODS OF USING SAME
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CITY: Madison STATE: Wisconsin

COUNTRY:

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US-08-222-177A-53
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MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION UNMBER: US/08/222,177A
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REGISTRATION UNMBER: 30,492
REGISTRATION UNMBER: 09865.601
TELEPHONE: (608) 831-2100
TELEPHONE: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/08222177A

Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dd-dA)n.(dd-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt ROSS & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Query Match
Query Match
Query Matches 36; DB 1; L
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                           COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
APPLICATION NUMBER: US/08/222,1771
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/341,562
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                                                                                        STREET: 8000 Exce
CITY: Madison
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                          US/08/222,177A
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genom:
IMMEDIATE SOURCE:

DNA (genomic)

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RESULT 14
US-08-222-177A-229
; Sequence 229, Application US/08222177A
; sequence 5582979
n=+ent No. 5582979
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; IMMEDIATE SOURCE:
; CLONE: mfdlrs
US-08-222-177A-53
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INFORMATION FOR SEQ ID NO: 5

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
           COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/341,562
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 11-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REGISTRATION NUMBER: 03,492
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (508) 831-2100
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sara, Chailes S.
REGISTRATION UNMER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 8000 Excel
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.1%; Score 36; DB 1; 1
100.0%; Pred. No. 0.00083
7ative 0; Mismatches 0
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TELEX:
TELEX:
INFORMATION FOR SEQ ID NO: 388:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd131s
US-08-222-177A-388
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US-08-222-177A-229
Search completed: March 29, 2000, 12:57:56
Job time: 32938 sec
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US-08-222-177A-388
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Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ANDRESCEPT. TOTALL.
                                                                                                                                                                                 Query Match 0.1%; Score 36; DB 1; Length 43; Best Local Similarity 100.0%; Pred. No. 0.00083; Matches 36; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 8000 Exce
CITY: Madison
STATE: Wisconsin
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ZIP: 53717-1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
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Page 8

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Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
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1 CACACACACACACACACA.....AGCCATACAGAGTGCGCCCC 30000
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               em_est1: * em_est3: * em_est4: * em_est4: * em_est5: * em_est6: * em_est6: * em_est6: * em_est11: * em_est6: * em_est11: * em_
gb_est24:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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n	Result
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80	sult Query No. Score Match Length DB ID
80 0.3	Query Match
103	Length
21	B
103 21 T77382	Ħ
T77382 yd72h12.r1	% esult Query No. Score Match Length DB ID Description

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DEFINITION
                                                                                                                                                                                                                                                                                                                                             ORGANISM
The WashU_Merck EST Project Unpublished (1995) other_ESTs: yd72h12.s1 Contact: Wilson RK Washington University School
                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

1 (bases 1 to 103)

1 (larse, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hillier, L., Clark, N., Dubuque, T., Lennon, G., Marra, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohifing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
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yd72h12.r1 Soares fetal
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AR503089
T52775
AQ006534
AAQ035225
E247004
AA335225
E347967
AA598741
AA07824
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AA144458
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liver spleen lNFLS Homo sapiens cDNA clone
to contains Alu repetitive element;, mRNA
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A0006534 CIT-HSP-
AA935225 oo66b11.s
A1045154 Homo sapi
F24490 HSP
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F244912.8
A598741 ae49912.8
B62983 CIT-HSP-669
B03985 CSRL-2115-9
F34634 HSPD29754 H
AA078242 TH1605 C
AA14448 mr80h05.6
AA14448 mr80h05.6
AA14448 mr80h05.7
AA960 RPCT11-3M4.
A058218 CRFL-116-3
AA79632 VS94603.7
AA79632 VS94603.7
AA79632 VS94603.7
AA79632 VS94603.8
AA79632 CSRL-1608.8
AA79630 CSRL-1608.8
AA79630 TG9560.8
AA745546 TY5600.8
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AA745760 TG7600.8
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AA500598 v190a02.
T52775 ya79d08.r1
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Best Local Similarity 100.0%;
Matches 80; Conservative
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103 TGAGAGTCTCACTCCACTGCAACCTCCCCCTCCTATATTCAAGTGATTCTCTTGCCTCA 44
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      The Washi-Merck EST Project Unpublished (1995)
Contact: Wilson RK Washington University School 4444 Forest Park Parkway, Box Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95)
1 (base
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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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R08388
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EST.
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Insert Size: 943
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Pred. No. 6.7e-16;
0; Mismatches 0;
                                                            School of Medicine way, Box 8501, St. Louis,
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1 (bases 1 to 89)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cione is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information. Insert Length: 727 Std Error: 0.00 Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                            AA500598 89 bp mRNA
v190a02.rl Stratagene mouse hea
IMAGE:919466 5', mRNA sequence.
AA500598
                                           Contact: Marra M/Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lc Tel: 314 286 1800
                                                                                                                      The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced
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Insert Size: 727
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clone is available royalty-free through LLNL; contact the
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/clone="IMAGE:127301"
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7 100.0%; Pr
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IMAGE:67887
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//dev_stage="13 day embryos"
//dev_stage="13 day embryos"
//deb_host="SOIR (Kanamycin resistant)"
//note="Organ: heart; Vector: pBluescript SK-; Site_1:
//note="Organ: heart; Vector: pBluescript SK-; Site_1:
//note="Organ: heart; Vector: pBluescript SK-; Site_1:
//note="Organ: heart; Vector: pBluescript Site_2: NhoI; Cloned unidirectionally. Primer:
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/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:919466"
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7 5' similar to contains Alu
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Pred. No.
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0.018;
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                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Other GSSs: CIT-HSP-2054B16.TR.1 CIT-HSP-2054B16.TR
CONTACT: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Adams, M.D., Rounsley, S.D., Field, C.E., Wible, C., Kim, U.-J.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J.,
Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
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CIT-HSP-2054B16.TF CIT-HSP
                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                         Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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/sex="Male"
                                                                                                                         /db_xref-"taxon:9606"
/clone-"2054B16"
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/clone="IMAGE:67887"
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/db_xref="GDB:504144"
                                                   /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:7057963"
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100.0%; Pred. No. 0.037;
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Homo sapiens genomic clone 2054B16
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Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797423.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Ilssue procurement: Christopher A. Moskaluk, M.D., Ph.D., Mic
Emmert_Buck, M.D., Ph.D.
Emmert_Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryotz; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 54)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NACI-CGAP (http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality Insert Length: 490 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
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                   /tissue_type="pooled germ cell tumors"
/lab_host="bH10B"
/lab_host="bH10B"
/note="vector: pT773D-Pac (Pharmacia) with a modified
/note="vector: pT773D-Pac (Pharmacia) with a Not I -
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1571133"
/clone_lib="NCI_CGAP_GC4"
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100.0%; Pred. No. 0.036;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sl sequence also available
This clone is available at the RZPD in Berlin
Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMÄNY
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12-MAR-1999
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  Eukaryota; Metazoa; (Eutheria; Primates; (bases 1 to 80)
Lanfranchi, G., Murar
                                                                                     F24490.1 GI:4810116
EST.
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F24490
                                                       Homo sapiens
                                                                                                                                           F24490
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; Metazoa; Chordata; Craniata; Vertebrata;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo saplens"
/clone="DKF2p434P234"
/clone_11b="434 (synonym: h
DH10B; sites Noti + Sali"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                            13 A;
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                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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    Muraro, T.,
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                           Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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Pred. No.
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  Caldara, F.,
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    Pacchioni, B.,
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    Pallavicini, A.,
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AUTHORS
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Best Local
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ae49g12.s1 Stratagene lung
IMAGE:950278 3' similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization genome Res. 6 (1), 35-42 (1996) 96276048
On Jun 5, 1998 this sequence version replaced gi:3188834.
                                                                                                                             Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos. Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Conserv
                           Tel: 314 286 1800
Fax: 314 286 1810
                                                       Washington University School of Medicine
                                                                                                 Unpublished (1997)
On May 18, 1995 th
                                                                                                                                                                                                Eutheria; Primates; Catarrhini;
1 (bases 1 to 89)
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University of Padua
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                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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ABI Chromatograms and other information are available on WWW
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(larity 100.0%;
Conservative
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est@watson.wustl.edu
lone is available royalty-free
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected streptavidin coated magnetic beads, ligated to
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/db_xref="taxon:9606"
/clone="s4000013A06"
/clone_lib="HM3"
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Pred. No. 0.087;
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l Similarity 100.0%;
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Ung-Jin Kim
Callech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA 91125, USA
Tel: 626 796 7066
Fax: 626 395 4901
Email: ung@ash.tree.caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 bp DNA GSS 21-JUN-1998 CIT-HSP-669F15.TP CIT-HSP Homo sapiens genomic clone 669F15, genomic survey sequence.
B62983
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1 (bases 1 to 102)
                                                                                                                                                                                                                                                                                                                                                                           end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim, U.-J., Adams, M.D. and Simon, M.I.
Determination of clone end sequences of human Bacterial Artificial
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/db_xref="taxon:9606"
/clone=11b="Stratagene lung carcinoma 937218"
/clone=11b="Stratagene lung carcinoma 937218"
/clone=11b="Stratagene lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SolR (kanamycin res
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                                                      /cell_type="Sperm"
/note="Yector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:5491647"
                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="669F15"
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1 (bases 1 to 58)

Evans,G.A., Burbee,D., Davies,C., Hominidae; Homo.

Jones,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S..,
Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M.,
Kupfer,K. and Garner,H.R.
Genomic Sequence Sampled Map of Chromosome 11

Unpublished (1996)

Ontagt: Warne Ga. Shane Broket
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                                               AI262095 80 bp mRNA EST 13-NOV-1998 qz28c05.yl NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2028200 5' similar to contains Alu repetitive element;contains TAR1 repetitive
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36; Conserv
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McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
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Seq primer: T7
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                         ;, mRNA sequence.
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/note="Vector: SCOs-1; Human Chromosome 11 specific cosmic
library prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, J1 t lothers
a 3 g 5 t lothers
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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1 (bases 1 to 84)
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1 (bases 1 to 84)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavici Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
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HSPD29754 HM3
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Location/Qualifiers
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1 (bases 1 to 80)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
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Fatima Bonaldo. "
75 C 24 g
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/clone_11b="NCI_CGAP_K1d11"
/lab_host="DH10B"
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                                                                                                                                                                                                                          contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A
Tel: 301402001
                                                                                                                                                                                                                                                                                                                                                                                                                                              Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L., Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D. 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries (Control of Control of Con
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36; Conservative
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96276048
On Jun 5, 1998 this sequence version replaced g1:3188981.
contact: Valle G.
                                                                                                                                                  Email: egreen@nhgri.nih.gov
Plate: 16 row: G column:
                                                                                                                                                                                                                 Fax: 3014024735
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ABI Chromatograms and other information are available on WWW
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/note "Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
oligo-dT-NotI primer
(5'-biotin-AACCCGGCTCGAGCGGCCGCTTTTTTTTTTTTTTTTT.3'). The
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
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0

0

Gaps

0

replaced g1:1292359

2A08,

Bethesda,

MD 20892

/db_xref="taxon:9606" /clone="7H16G05"

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ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
AA598741
                   BASE COUNT
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On May 18, 1995 this sequence version replaced gi:811447.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 89)

1 (bases 1 to 89)

1 (bases 1, National Control Cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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36; Conservative
              13
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/Gell_line="HeLa cell line; ATCC"
//lab_host="E. coll strain DHS alpha"
//lab_host="E. coll strain DHS alpha"
//note="Vector: pAMP10; cDNA, was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT).
From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA, selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."
a 0 c 45 g 44 t
                                                                                                                                                                                                                                                                                                                                                                            Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IndexE:950278"
/clone=1lb="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/tissue_type="lung carcinoma"
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1. .89
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/sex-"female"
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100.0%; Pred. No. 0.17;
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FEATURES

COMMENT

ORIGIN

Query Match
Best Local Similarity
Matches 36; Conserv Conservative 0.1%; Score 36; DB 36; Length 89; 100.0%; Pred. No. 0.17; tive 0; Mismatches 0; Indels 0,

Gaps

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Search completed: March 29, Job time: 11411 sec 2000, 06:25:57

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Run on:

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Maximum DB seq length: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:*
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12428.204 Killion cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311585 segs, 125096042 residues
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTGCAGTAGCTGCGACCTC......CAAAGTTTAGAGACATTTTT 20001
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                                                   T88080
Q34755
Q33755
V02178
Y0218139
T28139
T47081
Y5407
T93827
T93827
Q25032
T65788
V21577
                                                                                                                                                                                                                                                                                                                                Q33870
V19044
Q34050
Q27391
V37197
X16888
Q11762
V02146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q27391
Q33713
T65737
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Q33849
V19044
T65714
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                                                                     Nucleotide sequenc
Antitumoural phosp
Oligonucleotide sp
Repeat sequence fr
Heterologous block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microsatellite seq
Sequence of a micr
Repeat sequence fr
Inter-Alu specific
                                                                                                                                                                                                                       Human secreted pro
3' portion of cDNA
Microsatellite seq
Microsatellite seq
Human secreted pro
3' portion of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsatellite seq
Repeat sequence fr
Microsatellite seq
Alu PCR primer 1.
                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide se
Rat cytochrome P45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite seq
Alu PCR primer 1.
Repeat sequence fr
           Human GalR3
                             Synthetic Cholera
Human mitochondria
                                                                                                                                                                                Senescence-related Synthetic DNA prob
                                                                                                                                                                                                                                                                                                                                                      Self-complementary
                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite seq
Inter-Alu specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence fr
        primer
    RESULT
O33849
AC
O7
DT
O7
KW
FP
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                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0%;
Matches 48; Conservative
                                                                                                                                                                                                                         Q33849 standard; DNA; 70 BP.
Q33849;
Q2-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA26.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Result No.

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Pred. No. 1e-06; Mismatches

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Sequence	sequence	sequence	were a	probe.	chromo	contai	commer	human	repeat	marker	having	The in	7 (C - CA	Detect	WPI; 9	Weber	MARS-	04 - SEP	AL-APR	21-APR	10-DEC	US5582	Homo sa	linkage	PCR; po	Polymo	Repeat	T65735	T65735	135/c		;	7.4	2 62	41	40	2 6	37	36	ח
25	ב ב ב	ce has	mplifie	Over	some-sp	ning th	cial an	genetic	s, espe	s. Pri	the se	vention	711(06-0	ion of	7-04229	ĬĽ;	MARSH	1991;	. 586T-	-1989;	-1996.	979-A.	apiens.	e analy	olymera	rphism;	sequen		standard;			,	220	- 0		Ф С	> C	0	00	>
56 BP;	בים + אם י	has been de	d by pr	100 rep	ecific	e repeat	imal or	analys	cially:	mers bas	quence	relate		Detection of polymorphic	9/04.		ELEI'D CI	US-7543	US-3415	341562.			, CITT OHIO	sis; ger	se chain	repeat	ce from	64111	rd; DNA;			j	00.1		0.1	0.1	- F	, L	0.1	,
28 A	TIGE X	termi	mers	eat b	phage	t seq	plan	is si	for u	sed o	(dc-d	ל ל	10.9	phic			LINIC	77.		;			Some	etic	rea	sequ	מטוע פונדץ		56			,	2 2 2	00	0	00	ט ת	ı	0 0	>
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Νį	, Z	ar	579	Š	bra	ces	ree	S	'n	hes	@	18.	3 6	eti										sea	on;	07	14a					,	Q05003	737	V31	T47	717	T17	X01	1
6 BP; 28 A; 27 C; 0 G; 1 T;	NOTES WHICH CONCAINS	shown in T65704-797.	-T66047. Those clones	ere isolated. The inse	ies with a synthetic p	were isolated by hybri-	ling or pedigree analys	inkage analysis of gen	.g paternity or matern	markers. Primers based on these sequences can be used to detect these	-dT)n which can be use	lation of polymorphic	IIIOLS. dS	orm								US5582979-A.		e; animal; plant; bree	paternity; maternity;	enetic marker; primer;	I/"JUN"1997 (IIISE entry) Repeat sequence from polymorphic marker clone Mfd33.				ALIGNMENTS									
	s rue repear	This repeat	s where the repeat	erts from the clones	poly(dC-dA).(dG-d?	idisation of	sis. Clones	netic disease,	nity testing,	d to detect these	ed as genetic	repeat sequences	br mers											eding; locus;	digre	; amplification;							Sequence binding t	Analytical solid	Synthetic oligonuc	Synthetic DNA pro	Homo sapiens cio	Human mitochondria	Primer for mitocho	***************************************

Pred. No. 0.0
; Mismatches

0.00042; hes 0;

Indels

0

Gaps

0

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RESULT
V19044/c
ID V190
AC V190
DE ALU
DE ALU
KW CIRC
OS SYNT
SYNT
OS SYNT
OS SYNT
OS SACC
FP 09-J-
PF 09-J-
PF 09-J-
PF 09-J-
PF 09-J-
PF NO9-J-
PF PR 09-J-
PF PR 09-J-
PF Treco
PN WELL
FP PR O9-J-
OS SACC
OC C amplo
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PD 9-JUL-1996; W0-11478.

PR 09-JUL-1996; W0-U11478.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA (USSH) US DEPT HEALTH & HUMAN SERVIC
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PA (GENM) GENARK.

PA (GENM) GENNARK.

PA (GEM
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Best Local Similarity 100.0%;
Matches 41; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus.

W09213102-A.

06-AUG-1992.

15-JAN-1992; U00340.

15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alu PCR primer 1.
PCR; primer; ampli
circular yeast art
Synthetic.
Saccharomyces sp.
W09801573-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; amplification; Alu repeat sequence; vector;
plar yeast artificial chromosome; YAC; ss.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o. 0.00018;
o. 0.00018;
O; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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Query Match

Score 40;

DB 1;

Length 40

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PA (MARS) MARSHPELD CLINIC.

PA (MARS) MARSHPELD CLINIC.

PA (MARS) MARSHPELD CLINIC.

PR (MARSHPELD CLINIC.

PR (MARSHPELC CLINIC.

PR (MARSHPELD 
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US582979-A.
10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8640 TCGGCCTCCCAAAGTGCTGGGATTACAGGCTGAGCCACC 8679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1992: U00340.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
GEOTIGES M, Massey JM;
WFI; 92-284684/34.
Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                          Microsatellité sequence from clone TGLA400. PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss. Bos taurus. WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q34003 standard; DNA; 50 BP. Q34003; 02-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat sequence from polymorphic marker clone Mfd12.

Polymorphism; repeat sequence; genetic marker; priner; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4/c
T65714 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 TETETETETETETETETETETETETETETET 1
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39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.2%;
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PS Table 7; Page 331; 51/pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequence upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC oppirent). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC traits esp. in cattle, to allow selective breeding.
CS sequence 50 BP; 1 A; 2 C; 22 G; 25 T;
                                                                                                                                                                         pri gene mapping, and selective breeding ps Table 7; Page 371; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. CC by screening a library of bovine MoI DNA fragments of between CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. CC one out of 50 clones cross-hybridised. Assuming independent CC distribution of microsatellites and MooI sites, the frequency of (76)n >9 microsatellites in the bovine genome is estimated at >100, CC 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). CC on the sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp, microsatellite (using the program C opTIPRIM). The microsatellites may be used to identify individuals, C for parentage testing, and in the genetic mapping of economic trait craits esp. in cattle, to allow selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 38
Query Match 0.3
Best Local Similarity 100
Matches 38; Conservative
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Georges M, Massey JM;
WPI; 92-284684/34.
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Polymorphic bovine DNA markers - used in genetic identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of a microsatellite from clone TGLA58. PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
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                                                                                                                                                            BP;
                               0.2%;
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                                                                                                                                                     1 A;
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Score 38; DB Pred. No. 0.0 0.0 0; Mismatches
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                                                                                                                                                     0 C;
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Pred. No.
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                               DB 1;
0.001
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0.0017;
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                               .0017;
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                                                            Length 57;
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7513 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7550

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RESULT
T65736/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of polymorphic genetic markers of the form pletection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers placed mols. as primers placed mols. The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) grobe. Over 100 repeat blooks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat sequence is from the marker clone Mdf34 which contains the repeat sequence having the formula: (AC)4AT(AC)15.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 36
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21-APR-1989; 341562.
21-APR-1989; US-341562.
21-APR-1999; US-754351.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                   Ultterlinden AG, Vijg J;
WPI; 92-284683/34.
Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried fragments - onesisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                         T65736;
                                                                                                                                                                                       Synthetic.
W09213101-A.
 Claim 6; Page 6; 31pp; English
Primer PDJ33 is one of several
                                                                                                                        24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
                                                                                                                                                                                                                    Polymerase chain reaction; PCR; repetitive element;
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US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat sequence from polymorphic marker clone Mfd34.
Polymorphism; repeat sequence; genetic marker; primer; amplificati
PCR; polymerase chain reaction; paternity; maternity; human; pedig
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                        06-AUG-1992.
                                                                                                                                                                                                                                  Inter-Alu specific primer PDJ33.
                                                                                                                                                                                                                                                  27-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                 Q27391 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                      0.2%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Pred. No.
 primers which
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0.008;
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   are
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PA (GENM) JGENNARK.

PA (GENM) JGENNARK.

DR WPI; 92-28684/34.

DR WPI; 92-28684/34.

PT Polymorphic bovine DNA markers - used in genetic identification, price and selective breeding gene mapping, and selective breeding gene mapping, and selective breeding a gene mapping, and selective breeding PS Table 7; Page 213; 51/pp; English.

CT he sequence is that of a bovine microsatellite sequence obtd. by creaming a library of bovine microsatellite probe.

CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe.

CC one out of 50 clones cross-hybridised. Assuming independent clastribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, compared to information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence complification of the corresp. microsatellite (using the program complification of the corresp. microsatellite (using the program complification and in the genetic mapping of economic trait corresp. in cattle, to allow selective breeding.

CC correct category testing, and in the genetic mapping of economic trait correct c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 35
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Best Local S
Matches 35
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                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA134.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
Repeat sequence from polymorphic marker clone Mfd36. Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q33713 standard; DNA; Q33713;
                                                                                                                 T65737 standard; DNA; 45 BP T65737; [first entry]
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35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 0.2%; similarity 100.0%; 35; Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.017;
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RESULT 11
033870
AC 033870
AC 033870
DT 02-FBB
DE MICTOS
KW PCR; SW 90211a
PN W09211a
PN W09211a
PN W09211a
PN W09211a
PN W09216
PT 15-JAN
PR 15-JAN
PR 15-JAN
PR 15-JAN
CC 0750 en
CC 250 en
CC 15 sur
CC 15 sur
CC 150 c
CC 1760 po
DE Microsatellite sequence from clone TGLA272.

EM Microsatellite sequence from clone TGLA272.

EM Microsatellite sequence from clone TGLA272.

EM PCR; selection; primers; OPTIFRIM; breeding; cattle; parentage;

EM PCR; selection; primers; OPTIFRIM; breeding; cattle; parentage;

EM PCR; selection; primers; OPTIFRIM; breeding;

EM Sos taurus.

So Bos taurus.

So Bos taurus.

So Bos taurus.

PN W09213102-A.

PN W09213102-A.

PN W09213102-A.

PN W09213102-A.

PN W09213102-A.

PN GENMARK.

PI GENMARK.

PI GEOTGES M, Massey JM;

PR WPI; 92-284684/34 DNA markers - used in genetic identification,

PT POlymorphic bovine belective breeding

PS Table 7; Page 277; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by

CC Screening a library of bovine mbol DNA fragments of between

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised.

CC Tolone out of 50 clones cross-hybridised.

CC Tolon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pr Detection of polymorphic genetic markers of the form
pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
ps Disclosure; Column 9-10; 186p; English.

CC The invention relates to the isolation of polymorphic repeat sequences
CC The invention relates to the isolation of polymorphic repeat sequences
CC The invention relates to the solation of polymorphic repeat sequences
CC thaving the sequence (dC-dA)n. (dG-dT)n which can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing,
CC chuman genetic analysis such as linkage analysis of genetic disease,
CC commercial animal or plant breeding or pedigree analysis. Clones
CC commercial the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(GC-dA). (dG-dT)
CC probe. Over 100 repeat blocks were isolated. The inserts from the clones
CC were amplified by primers T65798-T66047. Those clones where the repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence has been determined are shown in T65704-797.
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CC sequence has been determined are shown in T65704-797.
CC sequence has been dete
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Best Local Similarity
Matches 35; Conserv
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21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC
Webber JL;
WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7526 TGTGTGTGTGTGTATGTGTGTGTGTGTGTGTGTGTGT 7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q33870 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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Pred. No.
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. 0.016;
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RESULT
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AC 030
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V19044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination yeast centromere, marker, and telomere and nucleic acid for recombination of the sequence for the PCR primer used in the Sxample 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the camplification of the Alu repeat sequence, which is used to amplification of the Alu repeat acids from the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of the mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1998.
09-JUL-1996; WO-U11478.
09-JUL-1996; WO-U11478.
(USSH) US DEPT HEALTH & HI
KOUDTING NY, LATIONOV VL, E
WPI; 98-110234/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10059 GCTCACGCCTGTAATCCCAGCACTTTGGGAGGCC 10092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7526
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See also Q33501-34437.
Sequence 54 BP; 1
                             (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA437. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                       06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces sp. WO9801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V19044 standard;
                                                                                                                                                                                                                                                                                                                      02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                       Q34050 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1998
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                                                                                                                                                                                                                 taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCACGCCTGTAATCCCAGCACTTTGGGAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%;
llarity 100.0%;
Conservative
        bovine DNA markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .larity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 40
                                                                                                                                                                                                                                                                                                                                                                       DNA;
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                                                                                                                                                                                                                                                                                                                                                                       86 BP
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VL, Perkins EL, Resnick MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
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     used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 35;
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0.016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.035;
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     genetic
                                                                                                                                                                                                                                                               cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 40
        identification
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RESULT V37197

15

V37197 standard; DNA; 80 V37197;

ВP

밁 ş

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PT gene mapping, and selective breeding
Table 7; Page 351; 517pp; English.

CT The sequence is that of a bovine microsatellite sequence obtd. by

CC Screening a library of bovine MboI DNA fragments of between

CC One out of 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of some sequence information for ca. 230 such bovine microsatellites

CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,

CC out of sequence information for ca. 230 such bovine microsatellites

CI summarised in the specification and indexed herein (see below).

CC were used to generate the required PCR primers for in vitro

amplification of the corresp microsatellite (using the program

CC optifrim). The microsatellites may be used to identify individuals,

CC for parentage testing, and in the genetic mapping of economic trait

CC loci, or genes involved the determinism of economically important

CC see also Q33501-34437.

SQ Sequence 86 BP; 11 A; 0 C; 40 G; 35 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 34
                                                                                  Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09213101-A.
06-AUG-1992; NL0018.
24-JAN-1992; NL-00018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
                  10059 GCTCACGCCTGTAATCCCAGCACTTTGGGAGGC 10091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91/c
Q27391 standard; J
Q27391;
Q27391;
Q27-JAN-1993 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2/-JAN-1993 (first
Inter-Alu specific p
Polymerase chain rea
Syntheti-
                                                                                                                                                                                                                                                   Claim 6; Page 6; 31pp; English.

Primer PDJ33 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can
                                                                                                                                                                                         be used to detect genetic variation.
See Q27389-Q27404 and Q33141-Q33144.
Sequence 35 BP; 8 A; 10 C;
                                                                                                                                                                                                                                                                                                                                                                                                               Detection of genetic variation by 2-D electrophoresis fragments - and hybridisation with labelled probes, or fragments consisting of inter-repeat sequences general
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uitterlinden AG, Vijg J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7513 GTGTGTGTGTGTGTGTGTGTGTGTATGTGTGT 7546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92-284683/34.
                                                                                  l Similarity
33; Conserv
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reaction; PCR; repetitive element;
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PE 13-ARR-1998; J03766.
PE 11-OCT-1996; J03766.
PR 117-OCT-1996; J0274855.
PR (MITU) MITSUBISHI CHEM CORP.
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PR (MITU) MITSUBISHI CHEM CORP.
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
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PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagawa H;
PI Fusini Y, Miyamoto E, Nemoto N, Yanagaw
Query Match 0.2%; Score 33; DB 1; Length 80; Best Local Similarity 100.0%; Pred. No. 0.064; Matches 33; Conservative 0; Mismatches 0; Indels
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Oligonucleotide sequence of the specification.
Genotype; phenotype; molecular evolutionary engineering;
functional biopolymer; virus; ss.
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WO9816636-A1.
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Search completed: March 29, 2000, 17:55:02 Job time: 50700 sec

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Result
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Perfect score:
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1: /cgn2_6/ptodata/]
2: /cgn2_6/ptodata/]
3: /cgn2_6/ptodata/]
4: /cgn2_6/ptodata/]
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Match
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1 AGTGCAGTAGCTGCGACCTC.....CAAAGTTTAGAGACATTTTT 20001
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10455.780 Million cell updates/sec
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              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-267-803B-87
US-08-267-803B-85
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US-08-454-557C-57
US-08-454-567-69
US-08-454-57-157
US-08-456-673C-57
US-08-456-673C-69
US-08-267-803B-47
US-08-267-803B-47
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US-08-27-177A-157
US-08-27-177A-157
US-08-454-557C-92
US-08-456-673C-92
US-08-456-673C-92
US-08-456-673C-92
US-08-456-673C-92
US-08-456-673C-92
US-08-456-673C-92
US-08-456-673C-92
US-08-113-646-44
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           Sequence 149, App
Sequence 27, Appl
Sequence 86, Appl
Sequence 57, Appl
Sequence 59, Appl
Sequence 69, Appl
Sequence 92, Appl
Sequence 92, Appl
Sequence 157, App
Sequence 92, Appl
Sequence 91, Appl
Sequence 92, Appl
Sequence 92, Appl
Sequence 91, Appl
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Sequence 92, Appl
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Sequence 93, Appl
Sequence 94, Appl
Sequence 97, Appl
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Sequence
Sequence
Sequence
                                            ; MOLECULE TYPE: DI
; IMMEDIATE SOURCE:
; CLONE: mfd33rs
US-08-222-177A-149
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; Sequence 149, Application US/08222177A
; Patent No. 5582979
 Query Match
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US-08-420-443-1	US-08-286-304-5	US-08-444-083-5	US-08-381-572-20	US-08-233-609-5	US-08-778-494B-114	US-08-664-596B-9	US-08-113-646A-40	US-08-287-164-2	US-08-222-177A-53	US-07-875-167-2	US-08-440-209-4	US-08-771-624B-10	US-08-771-624B-1	US-08-222-177A-175	US-08-433-505-9	US-08-677-944-2	US-08-776-944-13	US-08-776-944-12
		Sequence 5, Appli	Sequence 20, Appl	Sequence 5, Appli	Sequence 114, App	Sequence 9, Appli	Sequence 40, Appl		53,	Sequence 2, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 175, App		Sequence 2, Appli	Sequence 13, Appl	Sequence 12, Appl

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
NUMBER OF SEQUENCES: 460
                                                                                                                                                                        APPLICATION NUMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECHOMOUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 56 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/222,177A
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                             TYPE: nucleic acid
STRANDEDNESS: doub
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ZIP: 53717-1914
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Drive, Suite 401
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,802B

FILING DATE: 06-UNU-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mueting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 110.00030101

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1180AMATION:

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TELECOMMUNICATION 1180AMATION 1
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Best Local Similarity
Matches 43; Conserv
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TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 48; Conser
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                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7513 GIGITATORIAN TOTAL 
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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CITY: Minneapolis
STATE: MN
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5. 5741645
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                                                                                                                                                                                                                                                         5, Application US/08267803B 5834183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 43; DB 2; I ilarity 100.0%; Pred. No. 1.6e-06; Conservative 0; Mismatches 0;
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                                                                                   Ranum, Laura P.W.
Chung, Ming-yi
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                                                                                                                                                                           Harry T.
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Gene Sequence for Spinocerebellar Ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 54;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1217
INFORMATION FOR SED ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
myde: nucleic acid.
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US-08-22-177A-86/c
Sequence 86, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                           CITY: Madison
STATE: Wisconsin
COUNTRY: USA
CONPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dc-da)n.(dg-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: SI
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. Box CITY: Minneapolis STATE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 55458-1415
                                                                                                                                                                                                                  APPLICATION NUMBER:
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100.0%; Pred. No. 1.6e-06;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
                                                                                                                                                                                                             US/08/222,177A
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; IMMEDIATE SOURCE:
; CLONE: mfdl2rs
US-08-222-177A-86
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                                                ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 017957-000410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applic Patent No. 5712098
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SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT;
APPLICANT;
APPLICANT:
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REFERENCE/DOCKET NUMBER: 090
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Sara, Charles S.
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nes 39; Conservative
                                                                                                                                                                                                                           FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/632,673B FILING DATE: 16-APR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 39 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                     STRANDEDNESS:
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                                 nucleic acid
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Feder, John N.
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Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruddy, David
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DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
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100.0%; Pred. No.
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US-08-340-426D-57/c; Sequence 57, Application US/08340426D; Patent No. 5948634; GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne; APPLICANT: Wands, Jack R.
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Matches 3
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RESULT 6
US-08-454-557C-57/c
Sequence 57, Application US/08454557C
Parant No. 5830670
                                  Qy 12897 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 12934
                                                                                                                                                               US-08-454-557C-57
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                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludw19, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16299 CCTGGGTGCTCCACCTGGCACGTATATCTCTGCTCTTCC 16337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 New CITY: Washington STATE: D.C.
39 CCTGGGTGCTCCACCTGGCACGTATATCTCTGCTCTTCC 1
                                                                                                                                                                                                                                                                                                                                                                   NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                       . Similarity
38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO
                                                                     0.2%; Score 38; DB 3; Locality 100.0%; Pred. No. 9.2e-05; Conservative 0; Mismatches 0;
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NO
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                                                                                                       Length 60;
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                                                                       Gaps
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CORRESPONDENCE ADDRESS:

STREET: 1100 New CITY: Washington STATE: D.C.

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COUNTRY: U.S.A.

COMPUTER: 2005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIDAYING, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION INFORMATION:
NAME: LIDAYING, STEVEN R.
REGISTRATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
                           COUNTRY: U.S.A.

ZIP: 2005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CTANSIFICATION: 1MFORMATION:

NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-450-673C-57/c
Sequence 57, Application US/08450673C
Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVERTAL INFORMATION:

APPLICANT: de la Monte, Suzanne
APPLICANT: wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANDEDNES:

TOPOLOGY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match . O.2%; Score 38; DB 4; Local Similarity 100.0%; Pred. No. 9.2e-05; Local Similarity 100.0%; Pred. No. 9.2e-06; O; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: both PCT-US95-17111A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                 Matches
                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340
FILING DATE: 14 NOV-1994
ATTORNEY/ACENT INFORMATION:
NAME: LIDWY 5, YEVEN R.
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDITATIVE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
CLASSIFICATION:
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LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF ESQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                     Conservative
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100.0%; Pred. No. 9.2e-05;
7ative 0; Mismatches 0;
                                                                                                                             0.2%; Score 38; DB 6; L
100.0%; Pred. No. 9.2e-05;
ative 0; Mismatches 0;
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US-08-340-426D-57

Query Match Best Local S Matches 38

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NUMBER OF SEQUENCES: 1

ADDRESSEE:

STREET: 1100 New CITY: Washington STATE: D.C.

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; MOLECULE TYPE: US-08-469-802B-29
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                                                                                                                                                                                                                                            US-08-267-803B-47
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TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SECUENCES: 47
                                                                   Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                         Sequence 47,
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                           GENERAL INFORMATION:
                                                                               APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
cent No. 5834183
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: 612-305-1217
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MEDIUM TYPE: Floppy of
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ent No. 5741645
                                                  TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 85
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MN
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                                                                                                                                                                                                                                                                                                                 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 66
                                                                                                                                                                                                           7, Application US/08267803B 5834183
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612-305-1225
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Chung, Ming-yi
Zoghbi, Huda Y.
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                        Orr, Harry T.
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Mueting, Raasch, Gebhardt & Schwappach, P.A.
D. Box 581415
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; ; Pred. No.
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. 9.1e-05;
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US-08-454-557C-69/c
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 69, Application US/08454557C Patent No. 5830670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
INFORMATION FOR
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 New CITY: Washington STATE: D.C.
                                                                       REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McCormack, Myra H. REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20005-3934
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ZIP: 55458-1415
                                 TELEPHONE:
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DEDNESS: single
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                                                                                                         udwig, Steven R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzanne
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Pred. No.
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                                                                           .3840003
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. 9.1e-05;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: PC POS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 0609.3840002
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEG ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-340-426D-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OY 12897 GGTGAAACCCTGTCTGTCTAAAATACAAAAATTAGC 12934
Db 48 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 11
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LENGTH: 76 base pairs
TYPE: nucleac acid
STRANDENNESS: both
TOPOLOGY: both
US-08-454-557C-69
RESULT 14
US-08-450-673C-69/c
; Sequence 69, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
                                                                                                                                                          OY 12897 GGTGAAACCCTGTCTGTCTGTAAAATACAAAATTAGC 12934
Db 48 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 11
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US-08-340-426D-69/c
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Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5948634
GENERAL INFORMATION:
GENERAL INFORMATION:
de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20005-3934
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                                                                                                                                                                                                                                                    0.2%; Score 38; DB 4; Lilarity 100.0%; Pred. No. 8.9e-05; Conservative 0; Mismatches 0;
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Qy 12897 GGTGADACCCTGTCTCTACTADADATACADADATTAGC 12934
Db 48 GGTGADACCCTGTCTCTACTADADATACADADATTAGC 11
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PCT-US95-17111A-69/c
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Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 69, Application PC/TUS9517111A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 371-2500
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNET/ACENT INFORMATION:
NAME: Ludwig, Steven R. 203
REGISTRATION NUMBER: 36, 203
REFERENCE/DOKET NUMBER: 0608
TELECOMMUNICATION INFORMATION:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PLODS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CINSCIPLATION: $20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                   ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                               STREET: 1100 New
CITY: Washington
                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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100.0%; Pred. No. 8.9e-05;
ative 0; Mismatches 0;
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08/340,426

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FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REGISTRATION NUMBER: 371-2600

TELEPHONE: (202) 371-2600

TELEPHONE: (202) 371-2640

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

TOPOLOGY: both

PCT-US95-17111A-69

Query Match

O.2%; Score 38; DB 6; Length 76;

Best Local Similarity 100.0%; Pred. No. 8.9e-05;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 38; Conservative 0; Mismatches 12934

Qy 12897 GGTGAAACCCTGTCTCTACTAAAAATTACAAAAATTACC 12934

Qy 12897 GGTGAAACCCTGTCTCTACTAAAAATTACAAAAATTACC 11

Db 48 GGTGAAACCCTGTCTCTACTAAAAATTACC 11

Search completed: March 29, 2000, 17:48:08

Job time: 50350 sec
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Title:
Perfect score:
Sequence:
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length: 105
38
440
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US-08-852-495C-1_COPY_25000_45000
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13787.907 Million cell updates/sec
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em_est3: *
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gb_est2::

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Minimum Maximum

Searched:

9::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

N84707 J0579F Huma	C 1 51 0.3 70 25 N84707	25	70	0.3	51	_	n
tesult Query NO. Score Match Length DB ID Description	Ħ	8	Length	Query Match	sult Query No. Score Match Length DB ID	Result	Res
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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NB4707/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontar:
Tel: 4169788758
                                                                                                                                                                                                                                                                                        N84707 70 bp mF
J0579F Human fetal heart,
clone J0579 5' similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              N84707.1
                                  Fax: 4169785650
                                                                                                                                                                   (bases 1 to 70)
   il: liewcc@utcc.utoronto.ca
primer: GAAATTAACCCTCACTAAAGGG
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A1749123
AA078003
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AA280198
B80126
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AA578401
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AA555145
H67549
AQ319270
AA614379
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Lambda ZAP Express Homo sapiens cDNA
REPETITIVE ELEMENT ALU, mRNA sequence.
                                                                Toronto, Ontario,
                                                                                                                                                                                                                                                                                                                                                                                                                                       B48088 RPCIII 4N6.

B46088 Y130N05.12

R67088 Y130N05.12

R67088 Y130N05.12

R7414 Z030N05.11

R7415 Z030N05.11

R7416 Z
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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ORIGIN
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1 (bases 1 to 59)

2 (blases 1, Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Noubaga, T., Lacy, M., Le, M., Le, N., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rahlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Therry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA082835 59 bp mRNA
zn21g12.s1 Stratagene neuroepithelium
cDNA clone IMAGE:548134 3' similar to
element; mRNA sequence.
AA082835
AA082835.1 GI:1624910
EST.
                                                                                                                                                                                                                                                         Generation and analysis of 280,000 human expressed sequence Genome Res. 6 (9), 807-828 (1996) 97044478 on Sep 12, 1996 this sequence version replaced gi:1404580. Contact: Wilson RK washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 0.3%; Solution 0.3%; Solution 0.0%; 1 Similarity 100.0%; 1 S1; Conservative 0;
                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"10579"
/clone-"10579"
/clone-"10579"
/lab_host-"E. col1 XII-Blue"
/lab_host-"E. col2 XII-Blue"
/lab_host-"E. col4 XII-Blue"
/lab_host-"E. col7 XII-Blue"
/lab_host-"Yelfort
/lab_host-"E. col7 XII-Blue"
/lab_host-"E. col8 XII-Blue
/lab_host-"Yelfort
/lab_host-"E. col7 XII-Blue"
/lab_host-"Yelfort
/lab_host-"E. col7 XII-Blue"
/lab_host-"E. col7 XII-Blue
/lab_host-"E
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/clone_lib="Stratagene neuroepithelium NT2RAMI 937234"
/dev_Stage="Ntera-2/RA-MI neuroepithelial cells"
/lab_host="SOLR (Kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2
(Ntera-2/cl.01) precursor cells induced with Retinoic
Acid for 1 week, followed by 3 weeks in mitotic inhibitors
                                                                                                        /organism-"Homo sapiens"
/db_xref="GDB:3926650"
/db_xref="taxon:9606"
/clone="IMAGE:548134"
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1. .70
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8.4e-07;
thes 0;
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NT2RAMI 937234 Homo sapiens
contains Alu repetitive
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COMMENT
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Matches
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                                          18759
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Local Similarity 100.0%;
hes 47; Conservative (
TTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCACTCT 18805
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1 (bases 1 to 72)

NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On May 1, 1997 this sequence version replaced gi:2059395
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to
AI914923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -400P from Gibco
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI914923.1
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                                                                                                   Similarity
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                                                                                                                                                                                                     /note-"Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.35 kb. Tumor types include: mixed mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:2219558"
/clone_lib-"NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host-"DH10B"
                                                                                                   0.2%;
                                                                                               Score 47;
; Pred. No.
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Pred. No.
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2e-05;
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1.8e-05;
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Best Local Similarity
Matches 44; Conserv
                       AUTHORS
                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq_primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ535244 103 bp DNA GSS 18-
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 102)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P.
                                                                                                                                                                                                                                                    B48088 102 bp DNF
RPCI11-4N6.TP RPCI-11 Homo
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The Institute for Genomic Research
                                                                                                                                                              SSD
                                                                                                                                                                                   B48088.1
                                                                                                                                                                                                        genomic survey sequence. B48088
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
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AQ535244.1 GI:4846934
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                                                                                                                                       numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.2%; Score 44; DB 104; ilarity 100.0%; Pred. No. 0.00015; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
RPCII1 Human Male BAC Library"
1 27 C 27 g 18 t
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/db_xref="GDB:7621533"
/db_xref="taxon:9606"
/clone="RPCI-11-317H22"
                                                                                                                                                                                   GI:2600325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11"
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clone RPCI-11-4N6,
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Length 68; Indels

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30-MAY-1995

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MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lifo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: SP6
Class: BAC ends.
                                                                                                                                                              Contact: Shinji Radano Japan Science and Technology Corporation, NeuroGenes Project, Univ. of Tokai School of Med. Bohseldai, Isehara Kanagawa 259-1193, Japan Tel: 81-463-91-5095 Fax: 81-463-91-4993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                              On May 5, 1995 this sequence version replaced g1:798369
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUNA clones derived from 1 Mb of the Huntington's disease locus DNA Res. 3 (4), 239-255 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcript map of the human chromosome 4p16.3 consisting of 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 68)
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HUMSUPY036 Human brain cDNA Homo sapiens
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Use of BAC End Sequences for Sequence-Ready Map Building
Unbublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hadano, S., Ishida, Y., Tomiyasu, H., Yamamoto, K., Bates, G.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Similarity 100.0%; Pred. No.
43; Conservative 0; Mismatc)
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l. .os
/organism="Homo sapiens"
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/Cell_type-"Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
a 24 c 25 g 21 t
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/clone="RPCI-11-4N6"
/clone_lib="RPCI-11"
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/db_xref="GDB:7501469"
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9130h05.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:140793 3', mRNA sequence.
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1 (bases 1 to 96)

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On Apr 5, 1995 this sequence version replaced g1:760768
Contact: Wilson RK
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Unpublished (1995)
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                                      /Gev_stage="placenta obtained at birth (full term)"
//ab_host="PHIOB (ampicillin resistant)"
//ab_host="PHIOB (ampicillin resistant)
//ab_host="PHIOB (ampicillin resistant)
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/clone="033-00-1"
/clone_1ib="Human brain cDNA"
/tlssue_type="brain"
16 c 25 g 13 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:140793"
/clone_lib="Soares placenta Nb2HP"
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Location/Qualifiers
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Riikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Apr 14, 1993 this sequence version replaced gi:315343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                     /Clone_lb="Pancreatic Islet"
/(issue_type="pancreatic islet"
//lab_host="SoLr cells (kanamycin resistant)"
//note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
//note="Organ: pancreas; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:339537"
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/db_xref="GDB:1264911"
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AA555145
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Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98)
                                                                                                                                                                                                                                   H67549 98 bp mRNA EST 11-DEC-1995 yu68f10.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238987 3' similar to contains Alu repetitive element; contains
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On Sep 12, 1996 this sequence version Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                               repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
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/db_xref="taxon:9606"
/clone="IMAGE:1029654"
/clone_lib="NCI_CGAP_Prll"
                                                                                                                                                             GI:1114431
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/lab_host="DH10B"
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DO OCT 18, 1995 this sequence version replaced gi:1026289. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1810
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 102)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Other_GSSs: RPCIll-98B22.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                         AQ319270 102 bp DNA GSS 06-MAY-1999 RPCI-11-98B22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-98B22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: Promega -21ml3.
                                                                                                                                                                                                                                       Homo sapiens
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Insert Size: 174
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/clone="IMAGE:238987"
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/sex="Female"
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/db_xref="GDB:3864371"
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cive 0; Mismatches
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12 1 (bases 1 to 104)

13 NCI-GBAP http://www.ncbi.nlm.nih.gov/ncicgap.

14 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

15 Tumor Gene Index

16 Unpublished (1997)

17 Unpublished (1997)

18 Contact: Robert Strausberg, Ph.D.

17 Contact: Robert Strausberg, Ph.D.

17 Emert-Buck, M.D., Ph.D.

17 Emmert-Buck, M.D., Ph.D.

17 Emmert-Buck, M.D., Ph.D.

18 Emmert-Buck, M.D., Ph.D.

19 CDNA Library Preparation: M. Bento Soares, Ph.D.

19 DNA Sequencing by: Mashington University Genome Sequencing Center

10 Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lifo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seg primer: SP6
Class: BAC ends.
                                                                                           Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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RPCII1 Human Male BAC Library"
a 28 c 31 g 17 t
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                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Plke, Bethesda,
Tel: 301-402-4877
Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).

Plate: 15 row: d column: 10

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers
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On Dec 20, 1995 this sequence version replaced gi:1130959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Robey,P.G., Hotchkiss,R.N. and Francomano,C.A. SGAP: The Skeletal Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Libin Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : libin@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1129348"
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/lab_host="breast"
/lab_host="br
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                                                                                                                         /note="Organ:
22 c
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AI349123/c
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AA078003/c
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                                                                                                                                                                                                                  62 TTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: I.M.A.G.E. Consortium, I
DNA Sequencing by: Washington University Genome (
Clone distribution: NCI-CGAP clone distribution ifound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                       AA078003 105 bp mi
7H12D08 Chromosome 7 HeLa
7H12D08, mRNA sequence.
                                                                                                                                                                                                                                                                                        37; Conservative (
                                                                      AA078003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco.
Location/Qualifiers
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Homo sapiens
                                     EST
                                                     AA078003.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 72)
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                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
/note="Organ: lung; Vector: pAMP1; mRNA made from lung carcinoma tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. " 7 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2047646"
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ELECTRONS ELECTRONS CHARTHAIN; ROMINICAGE; PARCES
AUTHORS TOUCHMEN, JA. B. BURTGATG.G., Weintraub.L.A., Idol.J.R., Wang.L.,
ROBBINS; C.M., NUMESHAUM.JC., LOVELT, M. and Green E.D.
TITLE
2006 expressed sequence tags derived from human chromosome
JOURNAL Genome Res. 7 (3), 281-292 (1997)
WEDLINE
CONDENT: ETIC D. Green energy stanch
National Human Genome Research Institute/NIH
49 CONVENT Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201;
Fax: 3014024735
Emmil: egreenenburi.nih.gov
Plate: 1 row; D. column: 08
Seq primer: -21M13 (ABI).
FEATURES
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RESUL Q3385 ID AC DT · DE KW KW KW	Que Bes Mat Mat	SCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	000 00 0000 wwwwwaaaa
JT 2 033855 st 033855; 02-FEB-19 Microsate PCR; sele genetic n genetic n	Query Match Best Local S Matches 43 Matches 1111 7 20222 TTAT 1111 5 1 TTAT	UT 1 02-FEB-1993 Microsatell PCR; selectl PC	5 4 3 2 1 0 9 8 7 6 5 4 4 5 2 1 0 9 8 7 6 5 5 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
JIIT 2 955/c 033855 standard; DNA; 44 033855; 02-FEB-1993 (first entry Microsatellite sequence i PCR; selection; primers; genetic mapping; traits; Bos taurus.	imilarity ; Conser ;ATATATATA 	1 3855 standard; DNA; 44 3855; realection; primers; petic mapping; traits; petic mapping; doubt maker and solution of mapping M, Massey JM; persening and selectible 7; page 271; 517pp; e sequence is that of a central form of the constraint of the sequences upstream an increased in the spece sequences upstream and solution of microsate the petic summarised in the spece sequences upstream and solution of microsate the petic summarised in the spece sequences upstream and solution of microsate the petic summarised in the constraint of the co	00000000000
NA; 44 BP t entry) uence fror imers; Opr raits; amp	ttch 0.1%; Score 43; DB 1; al Similarity 100.0%; Pred. No. 0.0012; 43; Conservative 0; Mismatches 0 TTATATATATATATATATATATATATATATATATATA	RESULT 1 033855 ID 033855 standard; DNA; 44 BP. AC 033855; DT 02-FEB-1993 (first entry) DE Microsatellite sequence from clone TGLA261. KW per selection; primers; OPTIPRIM; breeding; cattle; parentage: W genetic mappling; traits; amplification; ss. OS Bos taurus NEW 9CR; selection; primers; OPTIPRIM; breeding; cattle; parentage: W genetic mappling; traits; amplification; ss. OS Bos taurus NEW 9CR; selection; primers; OPTIPRIM; breeding; cattle; parentage: W 9CR; selection; primers; oPTIPRIM; breeding PN 06-AUG-1992: W 909213102-A. PN 06-AUG-1992: W 909213102-A. PN 06-AUG-1992: W 909213102-A. PN 15-JAN-1991; US-642342. PN 15-JAN-1991; US-642342. PN 15-JAN-1991; US-642342. PN 16-JAN-1991; US-642342. PN 16-JAN-1991; US-642342. PN 16-JAN-1992; US-642342. PN 16-JAN-1992; US-642342. PN 16-JAN-1992; US-642342. PN 16-JAN-1991; US-642342. PN 16-JAN-1991; US-642342. PN 16-JAN-1992;	70 70 77 79 79 80 80 84 84 11 86 1
BP. y) from clone To OPTIPRIM; bz amplificatio	SCOTE 43; Pred. NO 0; Mismato 1,	prime relations and of the bridge and follows and follows and follows the bridge and follows at 100	Q34155 V30923 V99725 V79194 V26706 V32414 V37197 V3719
TGLA261. breeding;	3; DB 1; NO. 0.001 natches TATATATAT. 	a TGLA261. breeding; cattle; parentage; breeding; cattle; parentage; ation; ss. consider the frequence obtd. britised. Assuming independent of between a (TC)15 oligonucleotide probessed. Assuming independent of MboI sites, the frequency of or and indexed herein (see below ream of the microsatellite sequence of pcR primers for in vitro rosatellite (using the program by be used to identify individugenetic mapping of economic training of economically importantle preeding. G G; 22 T;	STN
cattle; p	Length 44 2; Indels 0; Indels ATA 20264	enetic identify par cattle; ca	
parentage	44; els 0;	itle; parentage; identification, sequence obtd. by of between nucleotide probe. independent the frequency of setimated at >100 bovine microsatell terein (see below). irosatellite sequen for in vitro sing the program identify individual ng of economic trai- mically important ing. T;	Sequence of a m: Human secreted Human adult test Staphylococcus of the control
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Minimum DB Maximum DB

seq

length: 8 length: 105 Total number of hits satisfying chosen parameters:

Searched: Word size :

Database :

N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Post-processing: Listing first 45 summaries

Title: Perfect score:

US-08-852-495C-1_COPY_40000_70000 30001

GTGTCACTCACGTTCAGCTA.....AACAACAGTTGCAGAATTGA 30001

Run on:

OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

March 29, 2000, 17:55:02;

Search time 599.46 Seconds (without alignments) 12521.290 Million cell updates/sec

Sequence: Scoring table:

OLIGO_NUC , Gapop 60.0 ,

Gapext 60.0

311585 seqs, 125096042 residues

Result No.

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Query Match

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Homo sapiens clone Homo sapiens clone 0000

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Q78635 Q78635 Q79780 V35728 V19045 T040045 T040045 T117035 T117035

Analytical sequence Analytical solid policies of the sequence alu PCR primer 2. Trypsin inhibitory Sequence of a micr Human mitochondria Human mitochondria Homo sapiens clone porcine reproducti DNA molecule encod Oligonucleotide sequence Human secreted pro y portion of cDNA PolydA 50mer prob Human secreted pro 1 Human GalR3 primer Lelystad virus pri Human secreted pro 3 portion of cDNA polydA 50mer prob Human GalR3 primer Lelystad virus pri Human secreted pro 3 portion of cDNA

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RESULT 3
Q24810/c
Q24810 standard; DNA; 63 BP.
AC Q24810;
DT 14-UUL-1992 (first entry)
DE Oligonucleotide containing RIF
KW DIAMOTOFOLATE reductase; Stable
KW DIAMOTOFOLATE reductase; Stable
KW DIAMOTOFOLATE reductase; Stable
KW DNA footprinting; (ATT)n bindid
KW Oligonucleotide affinity colum
SS Synthetic. Location/Quali
FT repeat_region 9.53
FT repeat_region 9.13
FT repeat_lif 9.11
FT repeat_lif 9.11
FT repeat_lif 9.11
FT repeat_unit 9.11
FT ROSE OF TAME-1992
PR 27-AUG-1991; U06119.
PR 27-AUG-1991; U06119.
PR 27-AUG-1991; US-573570.
PA (UYVE ) UNIV OF VERMONT.
PA (U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification,
year emapphing, and selective breeding
Table 7; Page 271; 517pp; English.
The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between
concept of 50 pwith an (Ac)15 and a (TC)15 oligonuclectide probe.
The sequence in the scross-hybridised. Assuming independent
cone out of 50 clones cross-hybridised. Assuming independent
cone of microsatellites and MboI sites, the frequency of
cone out of 50 clones cross-hybridised. Assuming independent
cone is summarised in the specification and indexed herein (see below).
The sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).
The sequences upstream and downstream of the microsatellite sequence
were used to generate the required PCR primers for in vitro
amplification of the corresp. microsatellite (using the program
of pripring). The microsatellites may be used to identify individuals,
confirming, and in the generatic mapping of economic trait
traits esp. in cattle, to allow selective breeding.
See also 033501-34437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral infection and cancer
Example 2; Page 42; 82pp; English.
Competition experiments using the DNAseI protection assay showed
that an oligonucleotide contg. 15 tandem ATT repeats was an
effective competitor for binding of the HeLa factor. This oligo was
used to prepare an oligonucleotide affinity column for purification
of RIF60 from Chinese hamster cells. The protein recognises and
binds to an (ATT)n motif in the diffr gene ori. It can also bind to
the yeast ARSI domain B. See Q22753 and Q24811.
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15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide containing RIP60 binding motif (ATT)15.
Dihydrofolate reductase; stably bent DNA; RIP60; RIP100; helicase;
DNA footprinting; (ATT)n binding factor; yeast ARS1;
oligonucleotide affinity column; ss.
                                                                                                                                                                                                                                      Replication initiator protein complex - comprises fractions for diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                         (UYRO ) ROCKEFELLER UNIV.
(UYVE ) UNIV OF VERMONT.
Heintz N, Heintz NH, Dailey LA, Caddle MS;
WPI; 92-096839/12.
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WPI; 92-284684/34.
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llarity 100.0%;
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/*tag= b
/note= "RIP60 binding motif"
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Pred. No.
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0.0012;
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Query Match
Best Local Similarity
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Best Local S
Matches 41
Synthetic
CA2112716-A.
01-JUL-1994.
11-DEC-1993; 112716.
31-DEC-1992; US-99520.
(USSU ) US SURGICAL CORP.
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Q71808 standard; DNA; 80 BP.
Q71808:
Q71808
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                                                                                                                                          Conservative
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071814 standard; DNA; 81 BP.
071814;
30-MAR-1995 (first entry)
Polyester coding sequence for insertion into

1 AATAATAATAATAATAATAATAATAATAATAATAATAA 41

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT New biocompatible medical devices and articles - using a lactic pri acid-glycolic acid polyester in which monomer units are pri acid-glycolic acid polyester in which monomer units are principled provided polyester genes given in Q71814-16 represent fragments of the Synthetic polyester genes given in Q71801-02. These fragments were commended in the production of the full length polyester gene in the plasmid contains the necessary initiator sequences and the contains the necessary initiator sequences and the contains the necessary initiator sequences and the contains the complete polyester coding sequence ligated in frame with the leader sequence. The expressed sequence represent synthetic contains the complete polyester coding sequence ligated in frame with the leader sequence. The expressed sequence ligated in frame with the leader sequence. The expressed sequence stop codons is reversed for the codons, UAA, UAG and UAA, one of these stop codons is reversed for the codons, UAA, UAG and UAA, one of these stop codons is reversed for the codons, UAA, UAG and UAA, one of these stop codons is reversed for the codons signal for the polyester. The remaining two stop codons are coded by UAA and UAG, respectively. Initiation of translation always starts at an AUG codon. This is accomplished through the use of a specially modified Met-thNAA modified be carry contained to remove the Met. Suppose browled to remove the Met. Suppose and scarry contains and screws.

CC devices, pins and screws.

CC devices, pins and screws.

6 C; 4 G; 24 T;
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31-DEC-1993; 112716.
31-DEC-1992; US-999520.
(USU) US SURGICAL CORP.
Gruskin EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27146 AATAATAATAATAATAATAATAATAATAATAATAATAA 27186
                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1995 (first entry)

SPORT-IC synthetic polyester gene 5' fragment and trpA initiator.

Synthetic gene; synthesis; polyester; a-amino acid analogue; clips

stop codon; stop signal; monomer unit; lactate; glycolate; staples

translation initiation; modified; Met-tRNAf; cyanogen bromide; pin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q71809 standard;
Q71809;
30-MAR-1995 (fi
                                                                                          misc_feature
                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                   misc_signal
                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                              co-polymer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            co-polymer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAATAATAATAATAATAATAATAATAATAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ene; synthesis; polyester; a-amino acid analogue; clips; stop signal; monomer unit; lactate; glycolate; staples; initiation; modified; Met-tRNAf; cyanogen bromide; pins; sutures; drug delivery device; screws; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                  /note-
19. .21
                                                                                       /note=
22. .9:
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 103
                                                              /*tag=
                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                             /*tag=
                                                                                             . 93
                                                                                                                                                                                                                                                                                                                                                          drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.1%;
                                                                                                                      "Start codon
                                                                                                                                                                                                           "trpA initiator
                               "Polyester gene 5' fragment"
                                                                                                                                                         Ծ
                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                       delivery device;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
0.0038;
                                                                                                                                                                                                                                                                                                                                                              screws;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         staples;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        clips;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pri New biocompatible medical devices and articles - using a lactic pri acid-glycolic acid polyester in which monomer units are rindividually and specifically determined represents a fragment of the plasmid psport ic which recontains the 5 fragment of the synthetic genes which encode polyesters, cc contains the 5 fragment of the synthetic genes which encode polyesters in 071801-02, under the control of the E. coli trpA transcription cc initiator and followed by FokI and HindIII restriction sites. A further fragment of the synthetic genes were ligated into psport Ic to give plasmid psport Id (see also Q71810-11), with the final fragment being coinserted in a third round of ligation to give psport Ic (see also Q71812-13). The E. coli trpA initiator sequence was used to express the full clampth sequences given in 071801-02 in an E. coli cell free medium. The expressed sequences represent synthetic genes which were used in the comming acid except Pro. Of the three stop codons, UAA, UAG and UGA, one cof the polyester. Lactate and glycolate are encoded by UAA and CC units of the polyester. Lactate and glycolate are encoded by UAA and CC UAG, respectively. Initiation of translation always starts at an AUG codon, therefore the first lactate of the chain may be encoded by an AUG codon. This is accomplished through the use of a specially modified CC resulting polymer is treated with cyanogen bromide to remove the Met. CC c-polymers produced in this manner may be used to produce sutures, staples, clips, drug delivery devices, pins and screws.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1994.
31-DEC-1993; 112716.
31-DEC-1992; US-99952
(USSU ) US SURGICAL C
                                                                                                                                                                                                                                                                              06-AUG-1992;
15-JAN-1992;
15-JAN-1991;
               gene mapping, and selective breeding
Table 7; Page 178; 517pp; English.
The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine mol DNA fragments of between
250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe.
One out of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and Morio sites, the frequency of
(T6)n >9 microsatellites in the bovine genome is estimated at >100,
000. The sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).
                                                                                                                                                                                               Georges M, Massey JM;
WPI; 92-284684/34.
Polymorphic bovine DNA markers -
                                                                                                                                                                                                                                                                                                                                                                         Microsatellite sequence from clone GBFSH.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               Q33621;
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gruskin EA;
                                                                                                                                                                                                                                                                                                                                      WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 94-272324/34.
                                                                                                                                                                                                                                                           (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q33621 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATAATAATAATAATAATAATAATAATAATAATAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-999520
                                                                                                                                                                                                                                                                              US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
   downstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                         used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; I
0.0035;
                                                                                                                                                                                                     genetic
 microsatellite sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 103
                                                                                                                                                                                                         identification,
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PA (GENM') GENMANA.

PI GROTYGES M, MASSEY JM;

DR WPI; 92-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification,

PT Polymorphic bovine DNA markers - used in genetic identification,

PT Polymorphic bovine DNA markers - used in genetic identification,

PT Polymorphic bovine DNA markers - used in genetic identification,

PT Polymorphic bovine DNA fragments of between company and selective breeding

PS Table 7; Page 178; 517pp; English.

CC The sequence is that of a bovine Microsatellite sequence of the frequency of company of microsatellites and Mbo! sites, the frequency of company of microsatellites and Mbo! sites, the frequency of company of the sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence complification of the corresp. microsatellite (using the program opping in the program opping of economic trait company of the microsatellites may be used to identify individuals, company of the microsatellites may be used to identify individuals, company of the corresp. microsatellite sequence of identify individuals, company of the program of the microsatellites may be used to identify individuals, company of the program of in the genetic mapping of economic trait sep. in cattle, to allow selective breeding.

Sequence 53 Bp; 20 A; 0 C; 0 G; 33 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESERVED TO THE PROPERTY OF TH
       RESULT
Q52732
ID Q5
AC Q5
DT 2C
DE Se
DE as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.1%;
Best Local Similarity 100.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Microsatellite sequence from clone GBFSH.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
Bos taurus.
Bos taurus.
WO9213102-A.
O6-BRE-1-7-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1992;
15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   were used to generate the required PCR primers for in vitro amplification of the corresp, microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also 033501-34437.

Sequence 53 BP; 20 A; 0 C; 0 G; 33 T;
052732 standard; DNA; 56 BP.
052733;
20-JUN-1994 (first entry)
Sequence of oligo nucleotide adaptor used for the synthesis of
asymmertically tailed plasmid primers for use in cloning libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                                                                                                                                         h 0.1%;
Similarity 100.0%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-642342.
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                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 0.0
BB
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. 0.0081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          в 1;
.0081
                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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RESULT 10
Q52734
ID Q52734
ID Q52734
AC Q52734
DE Sequen
DE ASYMME
KEY
FT M1SC_f
FT M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                  US5270185-A.
14-DEC-1993.
21-APR-1989; 341523.
21-APR-1989; US-341523.
21-AUG-1992; US-928856.
(HOFF) HOFFMANN LA ROCHE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           libraries
Claim 4; Figure 3A; 13pp; English.
Claim 4; Figure 3A; 13pp; English.
Claim 4; Figure 3A; 13pp; English.
The inventors claim an asymmetrically tailed plasmid primer comprising a cut,ds DNA plasmid contg. a functional origin of replication and at least one functional selection marker gene, one 3' terminus of which contains an oligo (dT) extension, the other 3' terminus of which contains an oligo (dC) or oligo (dG) extension terminated by a 3' phosphate group. More specifically, the asymmetrically tailed plasmid primer is produced by SacI and KpnI cleavage of plasmid pLP, and each terminus produced by the cleavage is joined to the complementary adaptor, which is Q52731 or Q52732.

Scomence 56 BP; 1 A; 6 C; 8 G; 41 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1993.
14-DEC-1993.
21-APR-1989; 341523.
21-APR-1989; US-341523.
12-AUG-1992; US-928856.
(HOFF) HOFFMANN LA ROCHE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Margolskee RF;
MPI; 93-404926/50.
Asymmetrically tailed plasmid primers - comprises cut,
double-stranded DNA plasmid, useful for producing cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asymmetrically tailed plasmid primer; Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q52734 standard; DNA;
Q52734;
Claim 5; Figure 3B; 13pp; English.
The inventors claim an asymmetrically tailed plasmid primer comprising a cut.ds DNA plasmid contg. a functional origin of replication and at least one functional selection marker gene,
                                                                                                                                wpi; 93-404926/50.
Asymmetrically tailed plasmid primers - comprises cut,
double-stranded DNA plasmid, useful for producing cloning
                                                                                                                                                                                       Margolskee
WPI; 93-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-1994 (first entry)
Sequence of oligo nucleotide adaptor used for the synthesis of asymmetrically tailed plasmid primers for use in cloning libraries.
Asymmetrically tailed plasmid primer; adaptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                              libraries
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (1. .4)
/*tag= a
/label= Sticky end
16. .56
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
/label=
16. .56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
/label=
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/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sticky end
                                                                                                                                                                                                                                                                                                                                                                                                     b
Sticky
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Sticky
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0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT
O78635
IO 2635
IO 26635
IO 278
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V05740
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11-MAY-1994; 107364.
11-MAY-1993; JP-109620.
17-DEC-1993; JP-318298.
(SUZU/) SUZUKI F.
(MITU ) MITSUBISHI KASEI CORP.
(MITU ) KONARA A, KONGO J,
SUZUKI J, Takahashi K, Yamada E
WPI; 94-350785/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chondrocytes and inhibits vascular endothelial cell growth of Example 4; Page 10; 34pp; English.

Q78635 and Q78636 are a pair of primers for Q78627-Q78632 which encode R65486-R65491 respectively, human chondromodulin-1 (CM-1), a chondrocyte growth regulator. CM-1 as part of a pharmaceutical compsn. with a carrier, excipient or solvent, can be used to stimulate chondrocyte growth. CM-1 also inhibits vascular endothelial cell growth, by promoting the differential potency of chondrocytes.

Sequence 61 BP; 2 A; 8 C; 8 G; 43 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminus of which contains an oilgo (dT) extension, the other terminus of which contains an oilgo (dC) or oligo (dG) extension the prime of plasmid primer is produced by EcoRI and HindIII cleavage of plasmid pUC19, and each terminus produced by the cleavage is joined to the complementary adaptor, which is 052733 or 05 sequence 56 BP; 1 A; 5 C; 8 G; 42 T;
11-DEC-1997.
06-JUN-1997: U09878.
07-JUN-1996; US-659224.
(GEMY) GENETICS INST INC
                                                                                                Homo sapiens. W09746683-A2.
                                                                                                                                         05-JUN-1998 (first entry)
Nucleotide sequence of the 3' portion of clone AS301_2.
Secreted protein; homology; antibody; immunoassay reagenutritional supplement; therapeutic activity; ds.
                                                                                                                                                                                                                                                 V05740
V05740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
EP-624645-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human chondromodulin-1 cDNA primer.
Chondromodulin-1; chondrocyte growth regulation;
vascular endothelial cell growth; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q78635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q78635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                          standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 0.1%; S
Similarity 100.0%;
39; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
0.015;
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                                                                                   Example 7; Page 21-22; 37pp; Japanese.

Example 7; Page 21-22; 37pp; Japanese.

The present sequence represents a probe used in an example from the present invention. The present invention describes an analytical solid phase method for detecting nucleic acids. The method comprises obtaining a base sequence which hybridises with the polynucleotide sequence of the target, and a set of probes immobilised on the solid phase via a linker which is enzymatically ligated during hybridisation. The product is used for the detection of specific nucleic acids. Possible fields of application include diagnosis of disease, detection of drug sensitivity, screening for appropriate transplantation organs, testing in the food screening for appropriate transplantation organs, testing in the food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13599
                                                                                                                                                                                                                                                                                                                                                                                           Analytical solid phase nucleic acid detection hybridisation probe 16.
Analytical solid phase detection; hybridisation; probe; target;
diagnosis; screening; disease; drug sensitivity; transplantation organized industry; food poisoning; ss.
                                                                screening for appropriate transplantation organs, testing industry to prevent food poisoning. A simple, quick method selectively detecting target in a mixed sample is obtained sequence 90 BP; 6 A; 14 C; 13 G; 57 T;
                                                                                                                                                                                                                                                 WPI; 98-271664/24.

Analytical solid phase for detecting nucleic acids - contains sequence which hybridises with polynucleotide sequence of transper, and a set of probes immobilised on the solid phase
                                                                                                                                                                                                                                                                                                    19-MAR-1998.
12-SEP-1997; J03232.
13-SEP-1996; JF-243720.
(MOLE-) LAB MOLECULAR BIOPHOTONICS
Abe S, Sato Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            great variety of therapeutic activities.
Sequence 87 BP; 79 A; 4 C; 4 G;
                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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Score 39; DB
Pred. No. 0.0
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NESULT 15
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ID V19045
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DE Alu PC
KW PCR: p
KW Circul
DS Sacha
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No. 1907, 100878.

PN M09746683-A2.

PD 11-DEC-1997; 100878.

PR O7-JUN-1997; 10
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Matches 39; Conserv
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09-JUL-1996; WO-U11478.
09-JUL-1996; WO-U11478.
09-JUL-1996; WO-U11478.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
KOUDTINA NY, Larionov VL, Perkins EL, Resnick MA;
WPI; 98-110234/L0.
Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination Example 1; Page 45; L17pp; English.
This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1998 (first entry)
Alu PCR primer 2.
PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1998 (first entry)
Nucleotide sequence of the 3' portion from clone AJ147_1.
Secreted protein; antibody: immunoassay reagent;
nutritional supplement; therapeutic activity; murine; calmegin; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Saccharomyces sp.
WO9801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V05728 standard; cDNA; 94 BP.
V05728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V19045 standard; DNA; 40 BP
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100.0%; Pred. No. 0.0
ative 0; Mismatches
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hes 0; Indels
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Matches 38
demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 9 A; 8 C; 19 G; 4 T;
                                                                           Similarity
                                                             Conservative
                                                                           0.1%;
                                                           0; Mismatches
                                                                         Score 38;
                                                                         DB 1;
                                                             0;
                                                                                         Length 40;
                                                             Indels
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Search completed: March 30, 2000, 00:58:13 Job time: 76091 sec

Page 7

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Title: Perfect score: Sequence:

US-08-852-495C-1_COPY_40000_70000 30001 1 GTGTCACTCACGTTCAGCTA.....AACAACAGTTGCAGAATTGA 30001

March 29, 2000, 17:48:08; Search time 340.37 Seconds (without alignments)
10552.676 Million cell updates/sec

OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

Scoring table:

OLIGO_NUC Gapop 60.0 ,

Gapext 60.0

214294 seqs, 59861574 residues

Minimum DB seq length: 8
Maximum DB seq length: 105

Post-processing: Listing first 45 summaries

Issued_Patents_NA: *

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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Total number of hits satisfying chosen parameters:

349160

Word size :

Result

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Query Match

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Description

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US-08-632-673B-1
US-08-241-465B-11
US-08-241-465B-12
US-08-231-565A-40
US-09-007-961-40
US-08-776-944-13
US-08-776-944-13
US-08-71-624B-1
US-08-440-209-4
US-08-440-209-4
US-08-113-646A-41
US-08-644-20-443-1
US-08-644-20-443-1
US-08-644-20-344-2
US-08-646-256B-3
US-08-664-256B-3
US-08-677-944-2
US-08-68-678-42
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US-08-68-68-68-42
US-08-68-68-68-42
US-08-68-678-978-42
US-08-68-678-978-42

1, Appl 42, Appl 40, Appl 40, Appl 40, Appl 13, Appl 13, Appl 14, Appl 14, Appl 14, Appl 17, Appl 17, Appl 18, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl

sequence sequence

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MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-632-673B-1
                                                                                                                                                                                   COMPUTER: IBM PC COMPACTIBLE
COMPUTER: IBM PC COMPACTIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/632,673B
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 030,223
REFERENCE/DOCKET NUMBER: 017957-000410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEPAX: (415) 326-2420
TELEFAX: (415) 326-2420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-632-673B-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tsuchi
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ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Feder, John N.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94111
                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Application US/08632673B 5712098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gnirke, Andreas
Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsuchihashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA
NO
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US-08-430-673C-91
US-08-450-673C-91
US-08-450-673C-91
PCT-US95-17111A-91
PCT-US95-17111A-91
US-08-450-673C-92
US-08-778-494B-116
US-08-592-98-1373
US-08-859-998-1373
US-08-859-998-1373
US-08-859-998-1373
US-08-859-998-1373
US-08-859-998-1373
US-08-859-998-1373
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91, Appl
91, Appl
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92, Appl
93, Appl
94, Appl
95, Appl
96, Appl
97, Appl
98, Appl
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99, Appl
99, Appl
99, Appl
99, Appl
90, Appl
91, Appl
91,
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INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 60 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid, Synthetic DNA
US-08-241-465B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-241-465B-11
                                                                                       RESULT 3
US-08-417-174-42
Sequence 42, Application US/08417174
Patent NO. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, JT.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08241465B
Patent No. 5719125
                                                                                                                                                                                                                                                                  Ouery Match 0.1%; Score 39; DB 2; L
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Akiko MORI
APPLICANT: EI YAMADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: BUJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20005
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Junko SUZUKI
Jun KONDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atsuko KOHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.1%; Score 39; DB 2; 1 larity 100.0%; Pred. No. 0.00033 Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yuji HIRAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujio SUZUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                             Length 60;
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                                                                                                                                                                                       US-08-231-565A-40
US-08-231-565A-40
IS-08-231-565A-40
Sequence 40, Application US/08231565A
PARTICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
APPLICANT: STEVEN A.
ITILE OF INVENTION: MELANOMA ANTIGENS AND
ITILE OF INVENTION: METHODS
ITILE OF INVENTION: METHODS
INTITLE OF INVENTION: METHODS
INTREE OF INVENTION: METHODS
INTREE OF SEQUENCES: 43
CORRESPONDENCE ADDRESS: 43
CORRESPONDENCE MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/417,174

APPLICATION NUMBER: US/08/417,174

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 43

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 2026-4124U:
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAN: (212) 751-6849

TELEX: 421792
INFORMATION FOR SEG ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYUEF: NUMBER: 1974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: US-08-417-174-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.1%; Score 38; DB 3; Length 58; Best Local Similarity 100.0%; Pred. No. 0.00066; Matches 38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13600 CITTITTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 13637
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TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                             STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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RESULT 5
US-09-007-961-40
; Sequence 40, Ap
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Best Local Similarity

Matches 38. Concern
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/231
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 421792
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: DOU
TOPOLOGY: UNKNOWN
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MELANOM THEIR UNTITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: NEW YORK
STATE: NEW YORK
                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               345 PARK AVENUE
                                                   (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEVEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAWAKAMI, YUTAKA; ROSENBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORGAN & FINNEGAN
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MELANOMA ANTIGENS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/231,565A
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US-08-776-944-12
                                                                              ;
ORGANELLE:
US-08-776-944-12
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1498
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 38; Conserv
Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12,
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                                                                                                                        MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9417211.1
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TULLY, GILLIAN
APPLICANT: SULLIVAN, KEVIN
TITLE OF INVENTION: NUCLEOTIDE SEQUENCING METHOD
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
NUTYON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEOTIDE STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 14-FE
                                                                                                                                                                                        STRANDEDNESS: SI
                                                                                                                                                                                                                                                                                                                                                   NAME: CRAWFORD, ARTHUR R. REGISTRATION NUMBER: 25,3
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, Application US/08776944 5925520
                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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   Conservative
                                                                                                             Homo sapiens
                                                                                             Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/776,944
14-FEB-1997
                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                        single
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              0.1%;
                                                                                                                                                                                                                                                                                                                            25,327
BER: 1498-92
              Score 38; DB 4; L; Pred. No. 0.00064;
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Pred. No.
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; L
. 0.00066;
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                             Length 70;
   Indels
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ORGANELLE: Mitochondrion US-08-776-944-13
                                                                                                                                                                                       RESULT 8
US-07-920-281C-25/c
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US-08-776-944-13
                                                                                                                                                                                                                                                                                                       MEDIOM TYPE: L'OPPY LISA
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,944
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9417211.1
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CRAMFORD, ARFHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1498-92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEPEAX: (703) 816-4106
TELEPEAX: (703) 816-4106
TELEPEAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                Sequence 25, Application US/07920281C
Patent No. 5739026
GENERAL INFORMATION:
APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.1%; Score 38; Best Local Similarity 100.0%; Pred. No. Matches 38; Conservative 0; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TULLY, GILLIAN
APPLICANT: SULLIVAN, KEYIN
TITLE OF INVENTION: NUCLEOTIDE SEQUENCING METHOD
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 75 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 22201-4714
    ADDRESSEE:
                                                                                                                                                                                                                                                                      ADDRESSEE:
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59255
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  Birch, Stewart, Kolasch & Birch
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US-08-113-646A-44/c
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                                                                                                                                                                                                                                                                                                                                            ; Sequence 44, ; Patent No. 5
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: PICKUP, David J.

APPLICANT: APTEL, Dhavalkunar

APPLICANT: ANTCZAK, James B.

TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/920
ETILING DATE: 13-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M.
NEGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEPAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
FEATURE:
ZIP: 2201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-005/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040-0747
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
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LOCATION:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                        STREET: 1100 NORU
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 TITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                         COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                            4, Application US/08113646A 5578468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                      1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.1%; Score 38; DB 2; I
ilarity 100.0%; Pred. No. 0.00062;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Semliki Forest Virus
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/note- "3' terminal sequence of cDNA expression
vector complementary to alphavirus genomic RNA"
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/771,624B
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
CLASSIFICATION NUMBER: US 60/009,090
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US-08-771-624B-1
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Patent No. 591423
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Best Local
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 10-AUG-1987 ATTORNEY/AGENT INFORMATION:
                                                            APPLICATION NUMBER: US 60 FILING DATE: 22-DEC-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rose, Samuel J.
APPLICANT: Ullman, Edwin F.
TITLE OF INVENTION: Homogen
TITLE OF INVENTION: of Nucl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
         NAME: RUSZALA, LOIS K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 31-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                    Deerfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                 Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08771624B
                                                                                                                                                                                                                                                                                                                                                                                  E: Behring Diagnostics GmbH, c/o Dade Behring Inc
1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin, Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patel, Rajesh D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA (genomic)
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INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homogeneous Amplification and Detection of Nucleic Acids
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US-08-771-624B-1
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JS-08-440-209-4
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Patent No. 5922857
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DAIL.
APPLICATION NUMBER: US 08/140,
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J
NAME: Janiuk, Anthony J
OTTORNEY/AGENT INFORMATION NUMBER: 29,809
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: COTELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TELEFAX: (847) 267-602
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                            MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Han, Jang
APPLICANT: Spaete, R:
TITLE OF INVENTION: I
TITLE OF INVENTION: INV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compation operating SYSTEM: PC-DC SOFTWARE: Patentin Ref. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, and Sacks P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 02210
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les 37; Conserv
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                                                                                                                                  TOPOLOGY:
                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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47) 267-6024
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                                                                                                                                                          single
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us 08/128,583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/440,209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/477,895
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0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 13
US-08-113-646A-41/c
US-08-113-646A-41/c
Sequence 41, Application US/08113646A
Patent No. 5578468;
Patent No. 557846108;
GENERAL INFORMATION:
                                                                                                                                                                                                                                     LENGTH: 50
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-420-443-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-420-443-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 0.1%; Score 37; D8 4; Length 40; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Query Match 0.1%; Score 37; DB 1; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08420443 Patent No. 5607834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Y. ROCKY TSAO
REGISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 0566
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIIM TYPE: 3.5" Diskette, 1.44 Mb
MEDIIM TYPE: 3.5" Diskette, 2.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/420,443
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: C. Bruce Bagwell
TITLE OF INVENTION: NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/990,298
FILLING DATE: 19921210
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fi
STREET: 225 F
CITY: Boston
STATE: Massacl
APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
APPLICANT: ANTCZAK, James B.
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02110-2804
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225 Franklin Street
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US-08-702-344-7/c
; Sequence 7, Application US/08702344
; Patent No. 5723315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTURNAL MILSON, MAN.

NAME: WILSON, MAN.

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 1579.

REFERENCE/DOCKET NUMBER: 1579.

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4000

TELEFX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs

TYPE: nucleic acid

""PANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
US-08-113-646A-41
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                                                                                                                           APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: McCoy, John
APPLICANT: Reviet, Edward
APPLICANT: Reviet, Lisa
APPLICANT: Recie, Lisa
APPLICANT: Merberg, David
APPLICANT: Merberg, David
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: ESCRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Gambridge
CITY: Cambridge
CITY: Cambridge
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/084,406
FILING DATE: 10-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
NAME: WILSON, MARY J.
NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.1%; Score 37; DB 1; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 37; Conservative 0; Mismatches 0
  COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
OPERATING SYSTEM: PC-DOS/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NOKE CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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1100 NORTH GLEBE ROAD
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       PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,344
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REGISTRATION INFORMATION:
TELEPHONE: (617) 498-8224
TELECAMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-8224
TELECAMUNICATION INFORMATION:
TORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-702-344-7
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US-08-702-344-22/c
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NAME: BIOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.1%; Score 37; DB 2; Length 69; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5723315
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CAPPLICATION DATA: PAPLICATION NUMBER: US/08/702,344 FILING DATE: CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vilki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08702344
linear
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; MOLECULE TYPE: CDNA
US-08-702-344-22
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Search completed: March 30, 2000, 00:47:59
Job time: 75541 sec

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Page 8

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
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(without alignments)
13848.486 Killion cell updates/sec
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Gapop 60.0 , Gapext 60.0
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em_est2: *
em_est3: *
em_est4: *
em_est5: *
em_est6: *
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em_gss8: * em_gss8: * em_gss9: * em_gss10: * em_gss11: * gb_gss11: * gb_gss13: *		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

B36140 HS-1038-A1-	65 81 B36140	81		0.2	58	c 1	ი
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Description	ij	DB	Length	Match	No. Score Match Length DB ID	Ö.	
				Query		Result	Re
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RESULT 1
B36140/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tagged Connectors
Unpublished (1997)
Contact: Mahairas GG, Zackrone KD,
University of Washington
Seattle, WA 98195
Tel: (206) 616-8744
                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Hominidae; Homo.

1 (bases 1 to 65)
Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Smithiras,G.G., Zackrone,K.D., Smith,T., Tipton,S., Smithoff,R., Abajian,C., Blanchard,A., West,A. and Econstruction of a Characterized Clone Resource for Geographics Generation and Preliminary Analysis of Sequencing: Generation and Preliminary Analysis of Sequencing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B36140 65 bp
HS-1038-A1-D06-MR.abi
sapiens genomic clone
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AR16332
AA844232
AA844232
AA80188573
AAQ282107
C257762
AL04766
AR80202641
AF378551
AA927559
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A
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CIT Human Genomic Sperm Library C Homo
Plate=CT 820 Col=11 RoW=G, genomic survy
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                                                                              Hood
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AA019576 ze61h02 s
AA019576 ze61h02 s
AA019576 ze61h02 s
AA0195772 c25772 Dict
A104760 DXF7p586K
AA824000 V493e09 K
AA028210 Homo sap1
A1638201 Homo sap1
A197855 HSPD07094 H
A397856 WFDD1084 x
E24490 HSPD1084 x
E24490 HSPD1084 x
E24490 HSPD1084 x
A1298440 FD1083 x
A1298440 FD1083 x
A129847 Tx05f09 x
A1915297 Tx05f09 x
A22977 Tx05f09 x
A22977 Tx05f09 x
A22974 Tx05f09 x
A23974 F0-29D 22 w
A249855145 N107904 s
A1636429 t103804 x
A1636455 x
A706655 x
A70665 x
A706655 x
A70665 x
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H61099 yr51612 r1
AU072757 AU072757
D20989 HDWGS01971
H67549 yr08f10.s1
R60869 yh08c10.s1
R60869 yh08c10.s1
A1653742 wb36h02.x
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AA082205 zn26h12.r
AA082205 zn26h12.r
AU038446 AU038446
N54156 yv63g11.s1
H61099 yr51c3g11.s1
AU072757 AU072757
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AA916300 on22c08
AI914923 tr27e08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey
                                                                                                                                                   , Schmidt,S.,
d Hood,L.E.
r Genomic
f 20,000 Sequence
                                                                                                                                                                                                                                                                                                          Mammalia;
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JOURNAL
COMMENT
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AA780764/c
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Best Local S
Matches 58
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Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 820 row: G column: 1
Class: BAC ends
High quality sequence stop: 65.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Frimates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Pheising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu, K. I., Wilson, R. Tan, F., Chellenberg, K., Wylie, T., Waterston, R. and Wilson, R. Washu, Wilson, R. Tan, F., The Martin, T., Walle, T., Waterston, R. and Wilson, R. Washu, Wilson, R. Tan, F., The Martin, T., Walle, T., Waterston, R. and Wilson, R. Washu, Wilson, R. Tan, F., Walle, T., Walle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
AA780764
AA780764.1
EST.
                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1407381.
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Fax: 314 286 1810
Email: estewatson wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: 40m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA780764 91 bp mRNA EST 05-FEB-1998 ac68f12.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:867791 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
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Similarity 100.0%; Pred. No.
58; Conservative 0; Mismatci
                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Stratagene fetal retina 937202"
/clone_lib="Stratagene fetal retina 937202"
/sex="mixed"
/sex="solx (kanamycin resistant)"
/lab_host="Solx (kanamycin resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
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E-Col1 DH10B"
a 18 c 10 g 12 t
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/db_xref="taxon.9606"
/clone="plate=CT 820 col=11 Row=G"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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. 5.4e-08;
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AA916300/c
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Best Local Similarity
Matches 53; Conserv
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source
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E 1 (bases 1 to 92)

S NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

On May 5, 1995 this sequence version replaced g1:797742.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGG
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                      Similarity 100.0%; 51; Conservative 0;
                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.2%; Scillarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1557422"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_bost="DH10B"
                                                                                                                                                                             /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " a 34 c 21 g 22 t
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NCI_CGAP_Lu5 Homo
contains Alu repet
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                                                                                                          0.2%;
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b; Pred. No. 7e-
0; Mismatches
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Homo sapiens cDNA clone IMAGE:1557422 3'
repetitive element;, mRNA seamence
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1.7e-06;
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7e-06;
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AUTHORS
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Matches 47
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H61099.1
                                                                                         EST
                                                                                                                                        H61099 95 bp mRNA yr51c12.rl Soares fetal liver: IMAGE:208822 5', mRNA sequence
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                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Primates; 1 (bases 1 to 72)
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                                                                                                            GI:1013931
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fetal liver spleen
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AUTHORS
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 95)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On May 1, 1997 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2219558"
/clone_1IMAGE:2219558"
/clone_1IMAGE:271958"
/clone_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 62; 1
                                                                                                                                                                                                                                                                                                                   EST
1NFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replaced g1:2059395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 72;
                                                                                                                                                                                                                                                                                                                      Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ph.D.,
                                                                                                                                                                                                                                                                                                                                                    06-OCT-1995
  Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 68)

1 (bases 1 to 68)

1 (chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., LeN., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Mohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Therry-Meg, J., Trevaskis, E., Underwood, K., Wohldman, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
On Sep 21 1992 this sequence version replaced g1:279312
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Insert Size: 1755
High quality sequence stops: 87
Source: IMAGE Consortlum, LLNL
Source: IMAGE Consortlum (Info@lmage.llnl.gov) for further information.
IMAGE Consortlum (info@lmage.llnl.gov) for further information.
Insert Length: 1755 Std Error: 0.00
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA082205 23-DEC-1997
ZNJ66hl2.rl Stratagene neuroepithelium NTRAMI 937234 Homo sap
CDNA clone IMAGE:548615 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Similarity
| 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., and Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                           AA082205.1
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Location/Qualifiers
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//lab_host="DH10B (ampicillin resistant)"
//lab_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia);
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia);
//natrand cDNA was primed with a Pac I - oligo(dT) primer
//natrand cDNA was primed with a Pac I adaptors
//natranded cDNA was ligated to Eco RI adaptors
//natrancia, digested with Pac I and cloned into the Pac I
//natrancia, digested with Pac I and cloned into the Pac I
//natrancia, digested with Pac I and Spleen Library
//went through one round of normalization. Library
//natrand constructed by Bento Soares and M.Fatima Bonaldo."
//natrand constructed by Bento Soares and M.Fatima Bonaldo."
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/clone="IMAGE:208822"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
/db_xref="GDB:3777953"
                                                                                                                                                                                                                                                                                                                                                                                                           GI:1624264
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Pred. No. 0.0011;
0; Mismatches 0
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AA082205/c
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VERSION
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AUTHORS
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ORGANISM
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Best Local S
Matches 43
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les 43; Conservative
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zn26h12.rl :
cDNA clone :
AA082205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Sep 12, 1996 this sequence version replaced gi:1397700. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrini; Hominidae; Homo.

1 (bases 1 to 68)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rikin,L., Mohifing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
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                                                                                 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu wARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                              On Sep 12, 1996 this sequence version replaced Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA082205.1
Washington University School of Medicine
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/db_xref="GDB:3927131"
/db_xref="GDB:3927131"
/db_xref="GDB:3927131"
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/clone_Ilb="Stratagene neuroepithelial cells"
/dev_stage="Netra 2/RA+MI neuroepithelial cells"
/lab_host="90IR (kanamycin resistant)"
/note="Yector: pBluescript SK'; Site_1: EcoRI; Site_2:
xho1; Cloned uniddirectionally. Primer: Oligo dT. NT2
(Ntera-2/Cl.Dl) precursor cells induced with Retinoic
acid for 1 week, followed by 3 weeks in mitotic inhibitors
(Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGCACGAGG 3' -3'
adaptor sequence: 5' CCGAGTTTTTTTTTTTTTTT 3'"
36 a de C 3 g 23 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 bp mRNA EST 23-DEC-1997
Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens
IMAGE:548615 5', mRNA sequence.
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. 0.0027;
ches 0;
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inhibitors

BASE COUNT

Query Match Best Local

REFERENCE AUTHORS

ACCESSION VERSION

KEYWORDS

ORGANISM

DEFINITION

RESULT AA082205

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REFERENCE
AUTHORS
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AU038446
LOCUS
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KEYWORDS
                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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Best Local Similarity
                                                                                                                                                                                             MEDLINE
                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                            JOURNAL
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                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU038446 93 bp mRNA EST 29-MAR-1999
AU038446 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSH729, mRNA sequence.
                                                                                                 University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                          AU038446.1 GI:3985199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.
                                                          Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                       On Dec 5, 1997 this sequence version replaced g1:2662913.
                                                                                                                                                                                                            DNA Res. 5 (6), 335-340 (1998)
                                                                                                                                                                                                                                development
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Dictyostellida; Dictyostelium
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further Seq primer: -28M13 rev2 from Amersham
                                                                                                                                      Institute of Biological Sciences
                                                                                                                                                          Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                      (bases
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                      1 to 93)
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/clone="IMAGE:548615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:3927131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.1%; Score 43;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 28;
0.0027;
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43; Conserv
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Email: est@watson.wustl.edu
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This clone is available royalty-free through LLNL; contact the
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101)
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/dev_stage="20 week-post conception fetus"
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//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Site_1: Pac I; Site_2: Eco RI;
//note="Organ: Site_1: Pac I; Site_1: Pac I;
//note="Organ: Site_1: Pac I; Site_2: Eco RI;
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/Clone="SSH729"
/clone_lib=m'Dictyostelium discoideum SS (H.Urushihara)"
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/dev_stage="slug"
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/db_xref="GDB:3796706"
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/clone="IMAGE:247460"
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; Pred. No. 0.0022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortum (info@image.llnl.gov) for further information.
Insert Length: 636 Std Error: 0.00
Seq_primer: m13 -40 forward
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

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/db_xref="GDB:3796706"
/db_xref="taxon:9606"
/clone="IMAGE:247460"
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Similarity

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Score 42; DB 24; Length 95; Pred. No. 0.0046;

Mismatches

Indels

0;

42;

Conservative

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REFERENCE
AUTHORS
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ORGANISM
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On Sep 21, 1992 this sequence version replaced gi:279312.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H61099 95 bp mRNA EST Yr51c12.r1 Soares fetal liver spleen INFLS IMAGE: 208822 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert 51ze: 1755
High quality sequence stops: 87
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1755 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 87.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
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                 44
          /organism="Homo sapiens"
/db_xref="GDB:3777953"
                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                              /clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                             /clone="IMAGE: 208822"
                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 1
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TITLE
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                               JOURNAL
                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jun 5, 1998 this sequence version replaced gi:3188495. Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba Sciences University of Tsukuba Salo Ten-nodai, Tsukuba, Ibaraki 305, Japan Email: d402hu@sakura.cc.tsukuba.ac.jp PROJECT - Dictyostelium discoideum cDNA project in Japan.
                                                                                                                                                                                         1 (bases 1 to 87)
Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.,
Yoshinari,H., Arimoto,J. and Matsubara,K.
Gene expression of human promyelocytic cell line HL60 before and
after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                                                            HUMGS01971 Human promyelocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU072757 73 bp mRNA EST 24-JUN-1999 AU072757 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSA765, mRNA sequence.
                                                                                                                                                          cDNA sequencing Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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Unpublished (1999)
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 73)
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                                                                                                                           Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Yoshinari, H., Arimoto, J. and Matsubara, K.
                                                                                                               institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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                                                                                            University
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="mp0383"
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/dev_stage="slug"
0 c l g 26 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="AX4"
/db_xref="taxon:44689"
/clone="SSA765"
                                                               Location/Qualifiers
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100.0%; Pred. No.
                                                                              Suita,Osaka 565,Japan
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0.011;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Riikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,F., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H67549 98 bp mRNA EST 11-DEC-1995 yu68f10.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238987 3', similar to contains Alu repetitive element;contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source: IMAGE Consortium, LLNL ;
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: Promega -21ml3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Insert Size: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Oct 18, 1995 this sequence version replaced gi:1026289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Marra,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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314 286 1810
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/note="Female, adult, cell_line
promyelocyte: "7 g 34 t
a 23 c 17 g 34 t
/tissue_type="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:238987"
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                           'sex="Female"
                                                                                                                                                                                                                                                                                    /clone_lib="Weizmann Olfactory Epithelium"
                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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Pred. No.
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. 0.0099;
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Matches Query Match Best Local &

41;

Conservative

0.1%; Score 41; DB 24; Length 98; 100.0%; Pred. No. 0.0092; 1tive 0; Mismatches 0; Indels

0; Gaps

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Local Similarity

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ACCESSION
VERSION
KEYWORDS
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ORGANISM
FEATURES
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Unpublished (1995)
On Apr 18, 195 this sequence version replaced gi:775532.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 1405
High quality sequence stops: 76 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lnln.gov) for further information.

Insert Length: 1405 Std Error: 0.00
                                                                                                                      tch 0.1%; Score 41; DB 22; Length 102; al Similarity 100.0%; Pred. No. 0.0091; 41; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 102)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucabar, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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yh08c10.s1 Soares infant brain 1NIB Homo
IMAGE:42595 3', mRNA sequence.
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Location/Qualifiers
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/db_xref="GDB:415136"
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Search completed: March 29, 2000, 20:38:58 Job time: 62592 sec

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Post-processing: Listing first 45 summaries
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AR051499 Sequence
D28457 Human mRNA
M87899 Human carci
L30907 Human STS U
AF087511 Homo sapie
L30907 Human STS U
AF087512 Sequence
L36838 Homo sapien
AR051522 Sequence 1
L36836 Homo sapien
AR051521 Sequence 1
L36836 Homo sapien
AR051522 Sequence 1
L36836 Homo sapien
L39139 Human STS U
AR051522 Sequence 1
L36836 Homo sapien
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AR051520 Scilland STS U
AR051525 Human low d
M36133 Human low d
M36133 Human low d
M36135 Human low d
M36355 Human low d
M36355 Human low d
M36355 Human STS U
AR05751 Human STS U
AR08751 Human STS U

Description

A08911 H.sapiens (M87896 Human carci G32655 A009130 Hum 250878 H.sapiens (AR051490 Sequence L30829 Human STS U

L36836 Homo sapien

29-SEP-1999

A08915 H.sapiens (M36134 Human alpha M36135 Human alpha G38859 TA50 Plasmo X78616 G.gallus ge L30306 Human STS U

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Patent: US 5830670-A 69 03-NOV-1998;
Location/Qualifiers
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1 Similarity 100.0%;
58; Conservative
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de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                disease
Patent: US 5830670-A 57 03-NOV-1998;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 60)
1 (bases, 3, and Wands, 3, R.
de la Monte, S. and Wands, 3, R.
Neural thread protein gene expression and detection of Alzheimer's
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AR051487.1 GI:5974851
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                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 48)
                                                                                                                                       HUMHH116 48 bp mRNA PRI 07-FEB-1999 Human mRNA for histone HID, 5'UTR (sequence from the 5'cap to start codon).
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Direct Submission Submitted (03-FEB-1994) to the DDBJ/EMBL/GenBank databases. Seishi
                                                                               Homo sapiens (library:HT-1080/pKA1) fibrosarcoma CDNA to mRNA, clone HP00474.
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Query Match
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Matches 48
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Homo sapiens
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates, Catarrhini; Hominidae; Homo.

1 (bases 1 to 104)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model
post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                              M87899
M87899.1 GI:174875
                                                                                                                                                                                                                                                                                                                                                                                                     HUMALCE272 104 bp ss-RNA PRI Human carcinoma cell-derived Alu RNA transcript,
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48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1994)
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Fax: 0427-49-7631
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larity 100.0%; Pred. No. 1.4e-13;
Conservative 0; Mismatches 0;
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/tissue_type="carcinoma"

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RESULT 6
AF087511/c
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HUMUT1543A/c
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Best Local S
Matches 41
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Best Local Similarity
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                                                                                                                                      39
                                                                                                                                      GAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGG
 AF087511 66 bp mRNA PRI 13-SEP-1999
Homo sapiens clone ENAC+22 epithelial sodium channel alpha subunit
(SCNNIA) mRNA, alternatively spliced, partial sequence.
AF087511
                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                Cycles Denaturation Annealing Extension C 10 sec. 56 C 10 sec. 72 C 20 sec. 30 56 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: CGAGACTTCCTTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 57)

Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens DNA.
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Human STS UT1543,
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41; Conservative
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16 c 13 g
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/db_xref="taxon:9606"
32. 50
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;; Pred. No. 3.1
0; Mismatches
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J. 7.3e-10;
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Best Local Similarity
Matches 36; Conserv
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c 10 sec. 56
56 C 10 sec.
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Oh,Y. and Warnock,D.G.
Direct Submission
Submitted (26-AUG-1998) Medicine,
Birmingham, AL 35294, USA
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 57)

1 (bases 1 to 57)

Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                    130907.1 GI:624443
STS; PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; sequence tagged site; tetranucleotide repeat.
                                                                                                  Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
primer A: CGAGACTCCGTCAAAGAAA
primer B: CCATTCCAACTTCTTCCATG
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Human STS UT1543,
                                                                                  End to Label: Primer A
                                                                                                                                                                                                                Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Oh, Y. and Warnock, D.G.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  Initial Denaturation: 94C 300sec
                                                                                                                                                                                                   Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                   White, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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20 c 2
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. 56 C 10 se
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/db_xref="taxon:9606"
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Pred. No. 3.1e-07;
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Best Local S
Matches 35
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                                                                                                                                                                                                                                                                                                                                                                                             HUMALUANCC 42 bp DNA PRI 08-OCT-1994
Homo sapiens 4000 year old remains from Nekht-ankh Alu repeat
fragment 12:4.
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1 (bases 1 to 85)

de la Montey.S. and Wands, J.R.

Neural thread protein gene expression and detection of Alzheimer's and the second 
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Sequence 92 from patent US 5830670.
AR051522
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Alleles: 5.
                                                                   Ancient DNA: extraction, characterization, molecular cloning, and enzymatic amplification
Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
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Location/Qualifiers
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/db_xref="taxon:9606"
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16 c 13 g
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 34; Conservative 0; Mismatches 0;
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l Similarity 100.0%; Pred. No. 3.5e-06;
34; Conservative 0; Mismatches 0;
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synthetic construct
artificial sequence.
1 (bases 1 to 35)
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de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's
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Sequence 91 from patent US 5830670.
AR051521
AR051521.1 GI:5974885
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Location/Qualifiers
1, .84
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                                                                                                                                                                                           METHOD OF DETECTING DNA SEQUENCE VARIATION PATENT: WO 9213101-A 3 06-AUG-1992; Location/Qualifiers

1. .35
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/isolate="4000 year old remains from Nekht-ankh"
/db_xref="taxon:9606"
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<1...>42
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10 c 17 g
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/db_xref="taxon:32630"
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JOURNAL FEATURES

REFERENCE AUTHORS TITLE

ACCESSION RESULT 8
AR051522/c
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SOURCE ORGANISM

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BASE COUNT ORIGIN

FEATURES

source

JOURNAL MEDLINE FEATURES

source

REFERENCE AUTHORS

TITLE

ACCESSION VERSION

SOURCE KEYWORDS

ORGANISM

RESULT 9 HUMALUANCC/c

DEFINITION

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RESULT 13
A68621
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E09140/c
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08-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                       "DETECTING METHOD FOR DNA ARRANGEMENT VARIATION";
Patent number JP 1995115999-A/3, 09-MAY-1995.
INGENII BV.
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Artificial sequences.
JP 1995115999-A/3
09-MAY-1995
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llarity 100.0%;
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/organism="unidentified"
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/note="Alu specific primer"
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HUMALUANCB
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                                                                                                                33 TTTGGGAGGCCGAGGCGGGCGGATCACGAGGTC
HUMUT578A 69 bp DNA
Human STS UT578, 5' primer bind, sequence tagged site.
L39139 L18336
L39139.1 G1:642101
STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 40)
Resnick,M.A., Larionov,V.L., Kouprina,N.Y. and Perkins,E.L.
TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
Patent: WO 9801573-A 15-JAN-1998;
US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMALUANCB 65 bp
Homo sapiens 4000 year
L36836
L36836.1 GI:556194
                                                                                                                                                                                                                                                                                                                     Ancient DNA: extraction, characterization, molecular cloning, enzymatic amplification proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%;
Conservative
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/isolate="4000 year old ro
/db_xref="taxon:9606"
/tissue_type="liver"
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/db_xref="taxon:32644"
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Nekht-ankh Alu repeat
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SOURCE ORGANISM

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Page 6
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Qy 15491 GTTGGCCAGGCTGGTCTCGAACTCCTGACCTCA 15523
Db 36 GTTGGCCAGGCTGGTCTCGAACTCCTGACCTCA 4
Search completed: March 30, 2000, 07:33:31 Job time: 101360 sec
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AUTHORS
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NAL Unpublished (1994)

Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
2161 Eccles Institute of Human Genetics
Salt Lake City, UT 84112

e-mail: sts@corona.med.utah.edu
primer A: AGTTCGAGACAGCCTGGC
Primer B: AGGTGGCAGAAAATCGCATC
End to Label: Primer A
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 5
Cycles Construction Annealing Cycles Denaturation Annealing Cycles Cycles Denaturation Annealing Cycles C
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 69)

Gerken, S.C. Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,

Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,

Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="STS UT578 5' end"
/evidence=experimental
26 a 16 c 14 g 13 t
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/db_xref="taxon:9606"
/map="19"
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Scoring table:

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Total number of hits satisfying
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30001
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                                                     Copyright
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                                                     GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd
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Alu PCR primer 1.
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Alu PCR primer 1.
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Polyester coding s
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Inter-Alu specific
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Inter-Alu s
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specific
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Q71808
ID Q7
AC Q7
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                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 41
05-MAR-1992.
27-AUG-1991;
27-AUG-1990;
                                                                                                                                                                                                                                                                                                                                              Example 2; Page 42; 82pp; English.

Competition experiments using the DNAseI protection assay showed that an oligonucleotide conty. 15 tandem ATT repeats was an effective competitor for binding of the HeLa factor. This oligo was used to prepare an oligonucleotide affinity column for purification of RIP60 from Chinese hamster cells. The protein recognises and binds to an (ATT)n motif in the dhir gene ori. It can also bind to the yeast ARSI domain B. See Q22753 and Q24811.

Sequence 63 BP; 19 A; 5 C; 6 G; 33 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1992 (first entry)
Oligonuclectide containing RIP60 binding motif (ATT)15.
Dihydrofolate reductase; stably bent DNA; RIP60; RIP100; helicase;
DNA footprinting; (ATT)n binding factor; yeast ARS1;
Oligonuclectide affinity column; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYRO ) ROCKEFELLER UNIV.
(UYVE ) UNIV OF VERWONT.
Heintz N. Heintz NH, Dailey LA, Caddle MS;
WPI; 92-096839/12.
                                                                                                                                                                                                                                Replication initiator protein complex - comprises 60 and 100 fractions for diagnosis, treatment and prevention of sepsis, viral infection and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9203479-A.
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                                                                                                                                                                                                                                                                        ch 0.1%;
l Similarity 100.0%;
41; Conservative
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US-573570.
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9. .11
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"RIP60 binding motif"
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Q34181
Q33804
Q33804
Q83951
T65733
Q34025
Q34025
Q341035
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Q341035
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Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                        DB 1;
0.0038;
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Word size Searched:

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PD 01-UL-1994; 112716.
PF 31-DEC-1993; 112716.
PR 31-DEC-1993; US-999520.
PR (USSU) US SURGICAL CORP.
PI Gruskin EA;
DR WPI; 94-272324/34.

PI acid-glycolic acid polyester in which monomer units are acid-glycolic acid polyester in which monomer units are racid-glycolic acid polyester in which monomer units are PI individually and specifically determined

Example 1; Page 45; 67pp; English.
CC encode polyesters given in Q71801-02. This fragment was ligated into the Klenow blunted sequences given in Q71801-02. This fragment was ligated into this synthetic fragment under the control of the E. coli trpA initiator sequence was used to express the sequences control of the E. coli trpA initiator sequence was used to express the sequences of polyesters derived from the a-amino acid analogues of an amino acid except Pro. Of the three stop codons, UAA, UAG and UGA, one of these control of the polyester. Initiation of the stop signal for the polyester. The except proceed by an acid analogues of an amino acid codon, therefore the first lactate and glycolate are encoded by UAA and CC waf, respectively. Initiation of translation always starts at an AUG codon, therefore the first lactate of the chain may be encoded by an CC wet is incorporated in the first position of the polymer chain. The composition of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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ol-JUL-1994:

ol-JUL-1994:

ol-JUL-1993: 112716.

Fig. 1-DEC-1993: US-999520.

A (USSU) US SURGICAL CORP.

Gruskin ED:

Gruskin ED:

New Diocompatible medical devices and articles - using a lactic gruskin ED:

New Diocompatible medical devices and articles - using a lactic gruskin ED:

New Diocompatible medical devices and articles - using a lactic gruskin ED:

New Diocompatible medical devices and articles - using a lactic gruskin ED:

New Diocompatible medical devices and articles - using a lactic gruskin ED:

The sequences given in 071841-16 represent fragments of the graduance given in 071841-10.

The sequences given in 071841-10.

Th
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Best Local Similarity
Matches 41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polysster coding sequence for insertion into pMAL-p2.
Synthetic gene; synthesis; polyester; a-amino acid analogue; clips; stop codon; stop signal; monomer unit; lactate; glycolate; staples; translation initiation; modified; Met-tRNAF; cyanogen bromide; pins; co-polymer; sutures; drug delivery device; screws; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             co-polymer; sutures; drug delivery device; screws; ds \mbox{\it Synthetic.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q71814 standard; DNA; 81 BP Q71814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
CA2112716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-1995 (first entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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. 0.0036;
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δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc template for the polypeptide leader. The resulting plasmid pMAL-2c contains the complete polypeptide leader. The resulting plasmid pMAL-2c contains the complete polypeter coding sequence ligated in frame with ct the leader sequence. The expressed sequences represent synthetic genes which were used in the synthesis of polysters derived from the cc armino acid analogues of an amino acid except fro. Of the three stop codons, UAA, UAG and UGA, one of these stop codons is reversed for the cc stop signal for the polyester. The remaining two stop codons are available for encoding the monomer units of the polyester. Lactate cand glycolate are encoded by UAA and UAG, respectively. Initiation of translation always starts at an AUG codon, therefore the first lactate cof through the use of a specially modified Met-tRNAH modified to carry carry the instead of Met. Alternatively, a Met is incorporated in the first position of the polymer chain. The resulting polymer is treated cuth cyanogen bromide to remove the Met. Co-polymer sproduced in this manner may be used to produce sutures, staples, clips, drug delivery constructions.
DR WPI; 94-273324/34.

DR WPI; 94-273324/34.

PI New biocompatible medical devices and articles - using a lactic acid polyester in which monomer units are acid-glycolic acid polyester in which monomer units are individually and specifically determined

PI individually and specifically determined

SE Example 1; Page 45; 67pp; English.

CC This sequence represents a fragment of the plasmid psporT Ic which contains the 5' fragment of the synthetic genes which encode polyesters, contains the 5' fragment of the synthetic genes which use sites A further initiator and followed by Fokl and Hinddill restriction sites A further fragment of the synthetic genes were ligated into psporT Ic to give plasmid psporT Id (see also Q71810-11), with the final fragment being conserved in a third round of ligation to give psporT ie (see also Q71812-13). The E. coli trpA initiator sequence was used to express the full length sequences represent synthetic genes which were used in the expressed sequences represent synthetic genes which were used in the corresponding to the synthesis of polyesters derived from the a-amino acid analogues of an
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Best Local Similarity
Matches 41; Conser
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01-JUL-1994.
01-DEC-1993; 112716.
31-DEC-1992; US-99520.
31-DEC-1992; US-99520.
(USSU ) US SURGICAL CORP.
GRUSKIN EA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )9
)9
071809 standard; DNA; 103 BP.
071809; (first entry)
30-MAR-1995 (first entry)
30-MAR-1995 (first entry)
spentric synthetic polyester gene 5' fragment and trpA initiator.
psppoRT-ic synthetic polyester; a-amino acid analogue; clips;
synthetic gene; synthesis; polyester; a-amino acid analogue; clips;
stop codon; stop signal; monomer unit; lactate; glycolate; staples;
stop codon; stop signal; monomer unit; lactate; glycolate; staples;
translation initiation; modified; Met-ERNAf; cyanogen bromide; plins;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2146 AATAATAATAATAATAATAATAATAATAATAATAATAA 2186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.1%; Score 41; DB 1; ilarity 100.0%; Pred. No. 0.0036; Conservative 0; Mismatches 0
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BP; 47 A;
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19. .21
/*tag=
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22. .93
/*tag= c
/note= "Polyester gene 5' fragment"
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"trpA initiator
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"Start codon"
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RESULT
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ID Q273
DC IDC Q273
DC INte
POLY
PN W092
PN W092
PN W092
PN W092
PN U1tt
DR WPI;
PT Cate
PT Frag
PT Cate
PT CC Lai
CC tran
CC diff
CC See
CC See
RESULT V19044 ID V1 AC V1 DT 28 DT 28 DE A1 CC VI KW PC CC SS SS SS SS SS
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Best Local S
Matches 41
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Best Local S
Matches 33
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24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid except Pro. Of the three stop codons, UAA, UAG and UGA, one of these stop codons is reversed for the stop signal for the polyester. The remaining two stop codons are available for encoding the monomer units of the polyester. Lactate and glycolate are encoded by UAA and UAG, respectively. Initiation of translation always starts at an AUG codon, therefore the first lactate of the chain may be encoded by an AUG codon. This is accomplished through the use of a specially modified MettRNAf modified to carry lactate instead of Met. Alternatively, a Met is incorporated in the first position of the polymer chain. The resulting polymer is treated with cyanogen bromide to remove the Met. Co-polymers produced in this manner may be used to produce sutures, staples, clips, drug delivery devices, pins and screws.

Sequence 103 BP; 58 A; 7 C; 9 G; 29 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 6; 31pp; English.

Primer PDJ33 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can be used to detect genetic variation.

See Q27389-Q27404 and Q33141-Q33144.

Sequence 35 BP; 8 A; 10 C; 11 G; 6 T;
                                                                                                                                                                                                                                                                                               1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                    Alu PCR primer 1.
PCR; primer; amplification; Alu repeat sequence; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2146
                                                                                                                             V19044 standard; DNA;
V19044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uitterlinden AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inter-Alu specific primer PDJ33.
Polymerase chain reaction; PCR; repetitive element;
Synthetic.
WO9213101-A.
  Saccharomyces sp
                                                                                                     28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227391 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-1993 (first entry)
                                                                                                                                                                                                                                                        35
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                                                                                                                                                                                                                                                                                               TGGCTCACGCCTGTAATCCCAGCACTTTGGGAG 1918
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                         0.1%;
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100.0%; Pred. No. 0.1
tive 0; Mismatches
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Pred. No.
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0.0034;
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination yeast telomere and nucleic acid for recombination.

Example 1; Page 45; 11/pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte adhesion
simplex; AIDS; modified;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              030397 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES. Kouprina NY, Larionov VL, Perkins EL, ReWPI; 98-110234/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9801573-A1.
15-JAN-1998.
09-JUL-1996; U11478.
09-JUL-1996; WO-U11478.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation;
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322 for forming triplex with HUMINTO2 target duplex.
Tyte adhesion protein; p150,95 alpha subunit gene; he
Tyte modified; HIV; RSV; HPV; malignancy; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/mod_base=
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13
                                           /mod_base=
/note= "OTH
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/mod_base=
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10
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/note= "OTHER= N6
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/mod_base=
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/mod_base=
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ER- N6
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ER- N6
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ER- N6
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herpes

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deoxyadenine'

deoxyadenine'

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deoxyadenine'

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deoxyadenine"

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deoxyadenine"

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Indels 6

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Gaps

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Length

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WO98U17.
15 JAN-1998.
15 JAN-1998; W11478.
F 09-JUL-1996; WO-U11478.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI KOUPTIN NY, LATIONOV VL, PERKINS EL, RESNICK MA;
PR WPI; 98-110234/10.
Preparation of yeast artificial chromosomes - by in vivo
Preparation using vector comprising yeast centromere, mar
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
V19044/c
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PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;

DR WPI, 92-217083/26.

PT New Oligomers contg. modified bases - which form a triplex with PT G-C doublet in a DNA duplex, for treating and diagnosing HIV, PT hepatitis, herpes, malignancy and inflammation

PT G-C doublet in a DNA duplex, for treating and diagnosing HIV, PT hepatitis, herpes, malignancy and inflammation

PT G-C doublet in a DNA duplex of inflammation

PT G-C doublet in a DNA duplex in the forming a triplex at the patient in the following and inflammation in the following in the following in the following a triplex at the following in the form an oraylose climer synthon. The linking gp. is oraylose (nucleotides have the 3 considered by in vitro systems and residue to form the dimer contains and inverted polarity region formed from an oraylose climer synthon. This additional modifications may render the oligomer stable conclease activity. The oligomer is able to inhibit gene expression, cas verified by in vitro systems.

Sequence 36 BP; 9 A; 0 C; 0 G; 27 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 30
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25-NOV-1991; U08811.
23-NOV-1990; US-641907.
18-JAN-1991; US-64382.
08-APR-1991; US-683420.
17-APR-1991; US-68544.
17-APR-1991; US-68544.
17-APR-1991; US-68534.
27-SEP-1991; US-68654.
27-SEP-1991; US-766733.
                                                                                                                                                                                                                             Synthetic.
Saccharomyces sp.
W09801573-A1.
                                                                                                                                                                                                                                                                                       Alu PCR primer 1. PCR primer 1. PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2158 AATAATAATAATAATAATAATAATAATAAA 2187
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                                                                                                                                                                                                                                                                                                                                            28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 ААТААТААТААТААТААТААТААТААТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.1%; Solution 0.1%; Solution 0.0%; 1 Similarity 100.0%; 1 30; Conservative 0;
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/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine
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"OTHER= N6 methyl-8-oxo 2' deoxyadenine'
                                                                                                                                                                                                                                                                                                                                                                                   ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score 30; DB; Pred. No. 5.5
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B 8

42

2460 AGTCTTGCTCTGTTGCCCAGGCTGGAGTGC 2489

Query Match
Best Local Similarity
Matches 30; Conserv

0.1%; Silarity 100.0%; Conservative 0;

Score 30; DB; Pred. No. 4.4
0; Mismatches

DB 1; 4.4;

Length 91;

Indels

0

Gaps

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CC A single-stranded DNA (or its complementary strand or the corresp. Claim 1; Page 2078; 2245pp; Japanese.

CC A single-stranded DNA) which comprises one of the 7837 "GS" sequences of double-stranded DNA) which comprises one of the 7837 "GS" sequences cc given in T19001-T26837 and which is able to hybridise to part of comprises one of the comprise of the comprise of the comprise of comprise of the comprise of comprise of the 
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Best Local Similarity
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yeast telomere and nucleic acid for recombination
Example 1; Page 45; 117pp; English.

This is the nuclectide sequence for the PCR primer used in the
amplification of the Alu repeat sequence, which is used to
demonstrate the processes described in the invention. It involves
the creation and use of circular yeast artificial chromosome (YAC)
to selectively clone specific nucleic acids from a background of
mixed nucleic acids by introducing the vector(s) into E. coli cells.

They can be used to rapidly isolate human DNA where only a part of the
sequence of DNA is known. Using the methods large fragments of DNA can
be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T26410;
06-DEC-1996 (first entry)
06-DEC-1996 (first entry)
Human gene signature HUMGSO8651.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsubara K, Okubo K;
WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126410 standard; cDNA to mRNA;
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5.4;
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V836407
ID 36407
ID 36407
ID 26407
ID 2
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                      Pr Assay for testing the carcinogenic properties of a test substance by introduction of a reporter gene expression vector containing a propertitive DNA sequence that is unstable in cancer cells repetitive DNA sequence that is unstable in cancer cells properties page 15; 103pp; English.

CC The present sequence represents an oligonucleotide used in the course of the construction of assay plasmids, which are used in the course of the construction of assay plasmids, which are used in the course of the construction. The specification describes an assay for testing the construction of assay plasmids, which are expression vector comprises of invention. The specification describes an assay for testing the carcinogenic properties of a test substance. The assay comprising a crepetitive DNA sequence which exhibits instability in cancer cells, confidently instability of the repetitive DNA sequence affects expression of the reporter gene, exposing the resulting cells to the test substance can anti-carcinogenic by comparing the frequency of reporter gene expression in cells which have not been exposed to the test substance. The assay can be used to identify human dietary components that protect against DNA contents of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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Q27391;
27-JAN-1993 (first e
Inter-Alu specific pr
    in the result cells which h be used to id instability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in amplifying inter-Alu regions of DNA. The amplified fragments then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method cabe used to detect genetic variation. See Q27389-Q27404 and Q33141-Q33144. Sequence 35 BP; 8 A; 10 C; 11 G; 6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repetitive sequence; ca
DNA instability; cancer
Synthetic
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08-APR-1998; G00869.

08-APR-1997; GB-007141.

(FOOD-) FOOD RES INST.
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WO9845476-Al.
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Oligonucleotide 1 used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INGE-) INGENY BV. Uitterlinden AG, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1992, NL0018.
24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schweizer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 6; 31pp; English.
Primer PDJ33 is one of several primers which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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WO9213101-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V83640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V83640 standard;
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    therefore
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primer PDJ33.
primer PCR; ;
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Pred. No. 20;
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    types
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                                                                                                                                                                                                                                                                                                                      PT Assay for testing the carcinogenic properties of a test substance - PT by introduction of a reporter gene expression vector containing a repetitive DNA sequence that is unstable in cancer cells pt Disclosure; Page 16; 103pp; English.

CC The present sequence represents an oligonuclectide used in the course of the construction of assay plasmids, which are used in the course of the construction of assay plasmids, which are used in the course of the construction. The specification describes an assay for testing the cc carcinogenic properties of a test substance. The assay comprises of introducing into cells a reporter gene expression vector comprising a repetitive DNA sequence which exhibits instability in cancer cells, whereby instability of the repetitive DNA sequence affects expression of the reporter gene, exposing the resulting cells to the test substance cand determining whether the test substance is carcinogenic or anti-carcinogenic by comparing the frequency of reporter gene expression in the resulting cells with the frequency of reporter gene expression in cells which have not been exposed to the test substance. The assay can be used to identify human dietary components that protect against DNA contribute to the scientific basis for a healthy diet.

Sequence 46 BP; 2 A; 6 C; 20 G; 18 T;
                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 28
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Best Local :
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08-APR-1998;
08-APR-1997;
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                                                                01-MAR-1999 (first entry)
01igonucleotide 1 used in the construction
Repetitive oligonucleotide; carcinogenic; }
DNA instability; cancer; diet; ss.
                                                                                                                         V83635;
15-OCT-1998.
08-APR-1998; G00869.
08-APR-1997; GB-007141
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DNA instability; can
                                       WO9845476-A1.
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V83641;
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18 A;
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human dietary component;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.1%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 19; Matches 28; Conservative 0; Mismatches
                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Page 17; 51pp; English.

095177 is a simple tandem repeat (STR) corresponding to the 2nd part of wgla2. The STR can be used for treatment and diagnosis in human and veterinary medicine, partic. for genetic characterisation, mapping, linkage studies and analysis/diagnosis of acquired disease alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q95177; standard; DNA; 57 BP.
Q95177; first entry)
08-FEB-1996 (first entry)
Simple tandem repeat (STR) corresponding to the 2nd part of wgla2.
Simple tandem repeat; STR; wgla2; treatment; genetic; diagnosis;
characterisation; mapping; linkage studies; analysis; alleles;
                                                               2467 CTCTGTTGCCCAGGCTGGAGTGCAGTGG 2494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1994; G02789.
21-DEC-1993; GB-026052.
21-DEC-1993; GB-026052.
Armour J, Jeffreys AJ;
WPI; 95-240682/31.
Identifying simple tandem repeat loci in DNA - by screening DNA library to enrich for fragments contg. the repeats before cloning and rescreening, also simple tandem repeats for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
WO9517522-A2.
                                                                                                                                                                                                                                                                                                         Sequence
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23
CTCTGTTGCCCAGGCTGGAGTGCAGTGG 50
                                                                                                                                                                                                                                                                                                             57 BP;
                                                                                                                              0.1%; Scilarity 100.0%; FC Conservative 0;
                                                                                                                                                                                                                                                                                                         7 A;
                                                                                                                                                                  Score 28;
Pred. No.
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                                                                                                                                  Mismatches
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                                                                                                                                  Gaps
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RESULT 15
Q33639
QY 18619 TGTGTGTGTGTGTGTGTGTGTGCA 18646
                                                                                                                                                                       PA (GINN') GENVARY.

PA (GINN') GENVARY.

PA (GINN') GENVARY.

DR WEJ: 92-286684/34.

PT Polymorphic bovine DNA markers - used in genetic identification,

PT gene mapping, and selective breeding

PT apile 7; Page 185; 517pp; English.

CC The sequence 1st that of a bovine microsatellite sequence obtd. by

CC conceoning a library of bovine MboI DNA fragments of between

CC one out of 50 clones cross-hybridised. Assuming independent

CC one out of 50 clones cross-hybridised. Assuming independent

CC offin >p microsatellites in the bovine genome is estimated at >100,

CC Offin >p microsatellites in the bovine genome is estimated at >100,

CC offin >p microsatellites in the bovine breath (see below).

CC offin sequences information for ca. 230 such bovine microsatellites

CC offin sequences upstream and downstream of the microsatellite sequence

CC were used to generate the required PCR primers for in vitro

amplification of the corresp. microsatellite (using the program of primary). The microsatellites may be used to identify individuals, complication and in the generate for in vitro

cc oppiprimy. The microsatellites may be used to identify individuals, complification, and in the generatic mapping of economic trait cross-complication, and in the generatic mapping of economic trait cross-complication of the corresponding of economic trait cross-complication of continuous elective breeding.

CC sequence 64 BP; 1 A; 2 C; 31 G; 30 T;
                                            Query Match 0.1%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 17, Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q33639 standard; DNA; 64 BP.
Q33639;
Q35639;
Q2-FEB-1993 (first entry)
Microsatellite sequence from clone MTGT13A.
PCR; selection; primers; OPTIPRIM; breeding; cat
genetic mapping; traits; amplification; ss.
Bos taurus.
Bos taurus.
H09213102-A.
Q6-AUG-1992.
15-JAN-1991; US-642342.
                                                                           DB 1;
17;
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                                                                                              Length 64;
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Search completed: March 30, 2000, 10:53:10 Job time: 111788 sec

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15 TGTGTGTGTGTGTGTGTGTGCA 42

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Result
No.
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Word size :
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                                                                                                                                                                              0000
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
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6: /cgn2_6/ptodata/
7: /cgn2_6/ptodata/
                                                                                                                                                                                                                                                                                                                                         Query
Match
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1 TTATTATGACAAAATTAAAT.....TACAGATACTCTTGCAGTTT 30001
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/5a_COMB.seq:*
/cgn2_6/ptodata/1/ina/5b_COMB.seq:*
/cgn2_6/ptodata/1/ina/5c_COMB.seq:*
/cgn2_6/ptodata/1/ina/5c_COMB.seq:*
/cgn2_6/ptodata/1/ina/5c_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcru9s_COMB.seq:*
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US-08-450-673C-92
US-08-450-673C-92
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US-08-450-673C-92
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	US-08-455-627-23	US-08-859-998-66	US-08-859-998-66	PCT-US95-17111A-91	US-08-450-673C-91	US-08-340-426D-91	-454-557C	-222-	US-08-222-177A-131	US-08-222-177A-421	US-08-222-177A-116	US-08-222-177A-424	US-08-222-177A-89	-222-177A-32	US-08-222-177A-346	US-08-222-177A-77	PCT-US95-17111A-67	US-08-450-673C-67
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ALIGNMENTS

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RESULT 1
US-08-454-557C-69
US-08-454-557C-69
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                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,557C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 514
                                                                                                   TELEPHONE: (202) 371-2
TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                    LENGTH: 76 base pairs TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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Query Match 0.2%; Score 58; DB 3; L Best Local Similarity 100.0%; Pred. No. 2.5e-10;

Conservative

0,

Mismatches

0

Gaps 27742

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Length 76;); Indels

27685 GCCCCGCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGGATG

63

Matches

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US-08-340-426D-69

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RESULT 3
US-08-450-673C-69
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                                                                                                                                                                                                                                                                                                              Patent No. 5948888
Patent No. 5948888
Patent No. 5948888
GENERAL INFORMATION:
    de la Monte, Suzanne
    APPLICANT: Wands, Jack R.
    APPLICANT: Wands, Jack R.
    1TTLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
    TITLE OF INVENTION: of Alzheimer's Disease
    TITLE OF INVENTION: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5948634
Patent No. 5948634
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
CORRESPONDENCE
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Ouery Match
Ouery Match
Dest Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 58; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,4261
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 0609.3840
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27685 GCCCCGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGGATG 27742
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                              STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C
                                                                                                                              COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20005-3934
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1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                               E: Sterne, Kessler, G
1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 base pairs
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                                                                                                                                                                                                                                                                                                    Kessler, Goldstein & Fox P.L.L.C ork Avenue, Suite 600
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TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
105-08-450-673C-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
PCT-US95-17111A-69
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
TYPE: pucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 69, Application PC/TUS9517111A GENERAL INFORMATION:
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Best Local Similarity 100.0%; I
Matches 58; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: Detection of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                 REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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STREET: 1100 New
CITY: Washington
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                                                                                                                                                                                       NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                                                                                              0609.3840002
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; TOPOLOGY: PCT-US95-17111A-69

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Sequence 57, Application v.,...
Sequence 57, Application v.,...
Sequence 57, Application v.,...
Patent No. 5948634
GENERAL INFORMATION: Gente, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
TITLE OF REGUENCES: 121
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US-08-454-557C-57
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NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 06.93
REFERENCE/DOCKET NUMBER: 06.99
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       Best
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APPLICANT: de la 1
APPLICANT: Wands,
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CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY AUTOCHMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                       Local
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100.0%; Pr
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Pred. No.
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Pred. No. 2.5e-10;
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40. 2.4e-09;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27685 GCCCCGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGG 27739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTOKNELY CHARMS: LUMMIN STEVEN R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 171-2600
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 06 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STREET: 1100 New Y
CITY: Washington
                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity es 55; Conserv
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1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 base pairs
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                                                                                                                                                       US/08/450,673C
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                                              0609.3840004
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            Goldstein & Fox P.L.L.C
e, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                            Version #1.25
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. 2.4e-09;
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RESULT 9
US-08-454-557C-92/c
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; Sequence 57, Application PC/TUS9517111A
; GENERAL INFORMATION:
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                                                                                                                                           Query Match
Best Local Sim
Matches 55;
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SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New York Avenue, Suit
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGRET INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                         Similarity 100
55; Conservative
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Wands, Jack R.
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                                                                                                                                                          0.2%; Score 55; DB 6; I
100.0%; Pred. No. 2.4e-09;
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                                                                                                                                                                                                                                                                                                                                        57:
                                                                                                                                           0;
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                                                                                                                                           Mismatches
                                                                                                                                             0; Indels
                                                                                                                                                                            Length 60;
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TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-454-557C-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-340-426D-92/c
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/454,557C
ETILING DATE: 30-MAY-1995
CIASCIPTICATION. S14
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GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 92, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 35; Conserv
                 COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLODS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                     APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC 14
                                                                                                                                                                                       STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                             ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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APPLICATION NUMBER:

US/08/340,426E

ATTORNEY/AGENT INFORMATION:

Ludwig,

Steven k

FILING DATE: 14 CLASSIFICATION:

14-NOV-1994

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Query Match
Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
                                                                                                                                                                                                                          NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/450,673C FILING DATE: 30-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC 14
                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
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                                                                                                                                               LENGTH:
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35; Conserv
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    Conservative
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Wands, Jack
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                                                                                                   both
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                                                                                                                                                                                                                (202)
                                                                                                                  hoth
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 0.1%; Score 35; DB
100.0%; Pred. No. 0.0
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 4;
Pred. No. 0.007
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                  DB 4; Length 85, 0.0071;
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    Indels
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   Gaps
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PCT-US95-17111A-92/c
                                                                                                                                                                                 Sequence 91, Application US/08454557C Patent No. 5830670
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 92, Application PC/TUS9517111A GENERAL INFORMATION:
                                                                                                                            GENERAL INFORMATION:
APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 171-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 21802 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC 21836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21802 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/34
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                        CORRESPONDENCE ADDRESS:
                                                                                        TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                           48 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: 1
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC
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                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Washington
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                    E: Sterne, Kessler, G
1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               both
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                    Kessler, Goldstein & Fox P.L.L.C
ork Avenue, Suite 600
                                                                           121
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                                                                                                                                               Suzanne
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. 0.0071;
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 85
                                                                                                                                                                                                                                                                                                                                                                  0;
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COUNTRY:

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION : 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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US-08-340-426D-91
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5948634

GENERAL INFORMATION:
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FITTLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: TIGHT STATES BY
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ZIP: 20005-3934
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US-08-450-673C-91
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Patent No. 5
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TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 91

SEQUENCE CHARRACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-450-673C-91
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                                                                                                                                                                                                                                                                                                                      ZIF: 20005-3934

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: Eloppy disk

COMPUTER: IBM PC compatable

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CHASTISTICATION: 530

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: LIGHTIS, Steven R.

REGISTRATION INFORMATION:

REFERENCE/DOCKET NUMBER: 0609.3840004

TELEPHONE: (202) 371-2600:

TELEPHONE: (202) 371-2600
                                                                           Query Match
Best Local Similarity
Matches 34; Conserve
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Best Local Similarity 100.0%; I
Matches 34; Conservative 0;
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                   2676 GCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACA 2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sterne, K
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44 GCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACA 77
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100.0%; Pred. No. 0.015;
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13817.943 Million cell updates/sec
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em_est8:*
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R07384 ye96c03.r1
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project.
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 83)
1 (bases 1 to 83)
1 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsokis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                               R07384 83 bp
ye96c03.rl Soares fetal
IMAGE:125572 5' similar
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AA2807629
AA077628
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AA0319270
AA032967
AA032967
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AA032864984
AA4815337
AA1708433
AA1708433
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AA627434
AA528266
AA182832
AA601685
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liver spleen lNFLS Homo sapiens cDNA cl
to gb:X57130_cds1 HISTONE HID (HUMAN);,
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AA280198 zt04b12:r
AI077628 by26f04:s
AA280198 zt04b12:r
AI077628 by26f04:s
AA28019270 RPCIII-98
F29274 HSPD19063
AA457423 aa86502:7
AU072757 AU072757
AA9077458 CITB1-E1-D25879 HUMG505672
AA907458 D102h06:s
B448914 RPCIII-4h2:2
C25772 C25772 Dict
C25772 C25772 Dict
C25772 PHUMG505672
AA551156 hK76d03:s
A1864984 wk06c11:x
AA515337 ng71c01:s
AA61153307:s
AA613153007:s
AA61379 na45611:1
AA809931 ac472692:s
AA517729 n147612:s
AA611655 n002a11:s
AA611655 n002a11:s
AA614479 np46c03:s
AA614479 np46c03:s
AA614479 np46c03:s
AA61466 z356609:s
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AA61479 np46c03:s
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T94466 ye35b02.r1
D44637 HUMSUPY036
AA584630 no12e10.s
AA019576 ze61h02.s
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AUTHORS
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Matches 54
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

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2 (bases 1 to 91)

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4 (bases 1 to 91
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54; Conserv
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Insert Size: 806
High qality sequence starts: 1 High qality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 806
Std Error: 0.00
Seq primer: M13RP1
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AA780764
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AEST.
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Fax: 314 286 1810
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/db_xref="GDB:478117"
/db_xref="taxon:9606"
/clone="IMAGE:125572"
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/sex="male"
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AA280198/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA280198
zt04b12.rl
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
                                                                                                                                                                                                                                                                                                                                                               The vector to vector length is 99
Insert Length: 622 Std Error: 0.00
Seg primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Sep 12, 1996 this sequence version replaced gi:1395022 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA280198.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 98)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (301) 496-1550
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: xhoi; Cloned unidirectionally. Primer: Oligo dr. Pooled retinal tissue. Average insert signer: bk; UnitZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"

a 33 c 24 g 19 t
                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:712127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Stratagene fetal retina 937202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:867791"
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                                                                                                                                                                                                            /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 bp mRNA EST 14-AUG-1997
NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712127 5'
contains Alu repetitive element;contains element MER22'
element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:1921755
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Pred. No.
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3.1e-06;
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Query Match Best Local

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Similarity

0.2%;

Score 53; Pred. No. Mismatches

DB 42; 1

Length 100

Indels

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Conservative

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Matches

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AI077628/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2153436.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI077628 100 bp mRNA EST 24-SEP-1998 oy26f04.sl Soares_senescent_fibroblasts_NbHSF Homo sapiens cDI clone IMAGE:1666975 3' similar to gb:x57130_cds1 HISTONE HID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Trace considered overall poor quality Insert Length: 820 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 100)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
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AI077628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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             double-stranded CDNA was size selected, ligated to Eco R adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

25 c 33 g 15 t
                                                                                                                                                                                             /tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pT7T3D (Pharmacia) with a modified
/note="vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="IMAGE:166975"
/clone=11b="Soares_senescent_fibroblasts_NbHSF"
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0; Mismatches
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AQ319270/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 102)

1 (Dases 1 to 102)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Batary, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ319270 102 bp DNA GSS 06-MAY-1999 RPCI11-98B22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-98B22,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
                                                                                                                                                                                                   F29274 91 bp mRNA EST 13-MAY-1999
HSPD19063 HM3 Homo sapiens cDNA clone s4000074G04, mRNA sequence.
F29274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of human BAC End Sequence Unpublished (1998)
Other_GSSs: RPCIll-98B22.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
AQ319270
AQ319270.1 GI:4052235
                                                                                                              Homo sapiens
                                                                                                                                                                            F29274.1 GI:4814900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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artment of Eukaryotic Genomics
Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                       0.1%;
llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:7537293"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="the"raxon:9682"
/clone="the"RPCI-11"
/clone="the"reft"
/clone="the"reft"
/clone="taxon:9682"
/clone="taxon:9882"
/cell_type="tymphocytes"
/cell_type="tymphocytes"
/note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
a 28 c 31 g 17 t
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; Pred. No. 0.00084;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by l sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996) 96276048 on Apr 7, 1998 this sequence version replaced g1:3034419. CONTACT: Valle G. CRIBI Biotechnology Centre
                                                                                                                                                                                                                                                          Dictyostelium discoideum.

Dictyostelium discoideum
Eukaryota, Dictyostelida; Dictyostelium.

1 (Dases 1 to 93)

Morio, T., Urushihara, H., Salto, T., Ugawa, Y., Mizuno, H., Yoshida, Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.

Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

The Dictyostelium developmental cDNa project: generation and analysis of expressed sequence tags from the first-finger stage
                                                                   DNA Res. 5 (6), 335-340 (1998)
99156227
On Dec 5, 1997 this sequence version replaced
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu&sakura.cc.tsukuba.ac.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Via Trieste 75, 35121 ABI Chromatograms and http://grup.bio.unipd.
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                                                                                                                                                                                                                                           development
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                                               d402hu@sakura.cc.tsukuba.ac.
T = 'Dictyostelium discoideum
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/db_xref="taxon:9606"
/clone="94000074604"
/clone_llb="HM3"
/sex="female"
       Location/Qualifiers
1. .93
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ns and other information
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.cDNA project in Japan'.
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g1:2662913

Yasukawa, H.,

Yoshida, M.,

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AUTHORS
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l Similarity
42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. See primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 95)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA457423 95 bp mRNA EST 06-JUN-1997 aa86b02.rl Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838155 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Nov 4, 1996 this sequence version replaced gi:1671271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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Eutheria; Primmates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                       /note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled retinal tissue. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor sequence: 5' CTGGAGTTTTTTTTTTTTTTTTT 3'" a daptor sequence: 5' CTGGAGTTTTTTTTTTTTTTTTTTT 3'"
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/strain="AX4"
/db_xref="taxon:44689"
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/clone_lib="Dictyostelium discoldeum SS
/dev_stage="slig"
2 c 1 g 33 t
                                                                                                                                                                                                                                                                                                                 /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:838155"
                                                                                                                                                                                                                                                                                               'lab_host="SOLR (kanamycin resistant)"
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1 (bases 1 to 92)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                     Unpublished (1997)
on Dec 20, 1995 this sequence version replaced g
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU072757 73 bp mRNA EST 24-JUN-1999
AU072757 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSA765, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AI932967
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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project
Location/Qualifiers
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Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3188495.
Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Dictyosteliida; Dictyostelium 1 (bases 1 to 73) Urushihara, H.
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.1%; Score 41; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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/clone="SSA765"
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/strain="AX4"
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4 Homo sapiens cDNA
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IMAGE:2457833
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Other GSSs: CITBI-21-2650p18.TF
Other GSSs: CITBI-21-2650p18.TF
CONTACT: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ626158 104 bp DNA GSS 16-JUN-1999
CITBI-E1-2650P18.TR CITBI-E1 Homo sapiens genomic clone 2650P18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                   end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                      Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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1 (bases 1 to 104)
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www-bio.llnl.gov/bbrp/image/image.html
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Similarity 100.0%; Pred. No. 0.015;
41; Conservative 0; Mismatches 0; Indels
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              /cell_type="sperm"
/note="Vector: pBeloBAC1; Site_1: EcoRI; Site_2: EcoRI;
Calfech Human BAC Library D"
28 c 22 g 42 t
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/clone=lb="NCI_CGAP_GBS4"
/tissue_type="poorly differentiated adenocarcinoma with
/tissue_type cell features"
/lab_host="DH10B"
                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2650P18"
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/db_xref="taxon:9606"
                                                                                          /sex="male"
                                                                                                        /clone_lib="CITBI-E1"
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Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1877755
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                  AA907458 97 bp mRNA EST 26-AUG-1998 0102h06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522331 3' similar to contains Alu repetitive element; mRNA sequence.

AA907458
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1 (bases 1 to 52)

Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K.

Global analysis of gene expression in colon mucosa: a large scale random cDNA sequencing analysis
Unpublished (1994)

Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, R.
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1 (bases 1 to 97)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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lontact: Okubo,K., Itoh,K., Yoshii,J., Yokou
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//db_xref="taxon:9606"
//clone="cm2335"
/clone=1lb="Human colon mucosa"
/clone=1db="Human colon mucosa"
/note="Adult male, tissue_type = colon mucosa "
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 97.
Location/Qualifiers
                      Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                          Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="IMAGE:1522331"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
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nes 40; Conserv
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Suzuki.K., Shimizu,H. and Urushiihara,H.
Sexual cDNA in D. discoideum(970724)
Unpublished (1997)
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C25772 Dictyostelium discoideum
discoideum cDNA clone FC-BB11, m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class:
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Email: d402hu@sakura.cc.tsukuba.ac.
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Dictyostelium discoideum
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/note="Vector: p
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/clone="FC-BB11"
/clone_lib="Dictyostelium discoideum FC (H.Urushihara)"
/clone_lib="Dictyostelium discoideum FC (H.Urushihara)"
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/clone="RPCI-11-4A12"
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/db_xref="GDB:7501163"
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1: gb_ba1:*
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9: gb_p1:*
9: gb_p7:*
10: gb_p7:*
11: gb_r0:*
11: gb_r0:*
13: gb_sts:*
14: gb_sts:*
15: gb_un:*
16: gb_v1:*
17: em_fun:*
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-6791.675 Million cell updates/sec
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     AR051499 76 bp DNA
Sequence 69 from patent US 5830670.
AR051499
AR051499.1 GI:5974863
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	gb_htg6:* gb_htg7:* gb_htg1:* em_htg1:* em_htg2:* em_htg3:* em_htg3:* em_hum5:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 (bases 1 to 76)

de la Monte, S. and Wands, J.R.

Neural thread protein gene expression and detection of Alzheimer's disease
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Unknown.
                                                                                                                                                                 Sequence 159 from patent US 5869241.
AR032547
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de la Monte, S. and Wands, J.R.
Neural thread protein gene expression and detection of Alzheimer's
                                       1 (bases 1 to 48)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Method of determining DNA sequence preference of a DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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Sequence 57 from patent
AR051487
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US 5869241-A 159 09-FEB-1999;
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   48 GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCTGCCCCCC
                                                                                                                                                               Unclassified. 48)

1 (bases 1 to 48)

1 (bases 1 to 48)

Edwards, C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M. Screening assay for the detection of DNA-Dinding molec Patent: US 5726014-A 159 10-MAR-1998;

Location/Qualifiers
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Sequence 159 from patent
190961
190961.1 GI:3936477
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Sequence 159 from patent US 5578444.
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Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.

Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.

Sequence-directed DNA-binding molecules compositions and methods

Patent: US 5578444-A 159 26-NOV-1996;

Location/Qualifiers
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1 Similarity 100.0%;
47; Conservative 0;
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Sequence-directed DNA-binding molecules compositions and methods
Patent: US 5578444-A 170 26-NOV-1996;
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Location/Qualifiers
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Location/Qualifiers
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Edwards,C.A., Cantor,C.R., Andrews,B.M.,
Sequence-directed DNA-binding molecules (
Patent: US 5578444-A 167 26-NOV-1996;
Location/Qualifiers
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Edwards, C.A., Cantor, C.R., Andrews, B.M., Turion Method of determining DNA sequence preference
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Sequence 167 from
AR032555
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Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 167 10-MAR-1998;
Location/Qualifiers
1. 46
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  Sequence 169
129297
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Method of determining DNA sequence preference of a DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent:
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Sequence 169 from patent
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190971.1 GI:3935441
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Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 169 10-MAR-1998;
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.

Sequence-directed DNA-binding molecules compositions and methods

Patent: US 5578444-A 169 26-NOV-1996;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 79)
Schichman,S.A., Caligiuri,M.A., Strout,M.P., Carter,S.L., Gu,Y., Canaani,E., Bloomfield,C.D. and Croce,C.M.
ALL-1 tandem duplication in acute myeloid leukemia with a normal karyotype involves homologous recombination between Alu elements Cancer Res. 54 (16), 4277-4280 (1994)
                                                                                                                                                                                                                               S73203 79 bp DNA
ALL-1 (tandem duplication)
Genomic Mutant, 79 nt).
S73203
S73203.1 GI:685048
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[human, acute myeloid leukemia patient,
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GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 155288] from the original journal article. This sequence comes from Fig. 3a.

Map location: 11.

Location/Qualifiers
1. .79

/organism="Homo sapiens"
/db_xref="taxon:9606"
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    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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RESULT 2 T63871; tandard; DNA; 48 ID T63871; tandard; DNA; 48 AC T63871;

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Query Match 0.2%; Score 48; DB 1; Le Best Local Similarity 100.0%; Pred. No. 9.7e-05; Matches 48; Conservative 0; Mismatches 0;

Length 48; 5; 0; Indels

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W09414980-A. 20-DEC-1993; US-19 23-DEC-1993; US-19 (GENE-) GENELABS T Andrews BM, Canto WPI; 94-234711/28. Sequence-directed pharmaceuticals an Claim 28; Page 291 A DNA protein-bind 11braries of synth to bind DNA test s number of test seq adjacent to a defi of mols to these of the protein mol binds the test seq adjacent to a defi factors (e.g. TRII from DNA sequences transcription fact the sequences in Q (typically TATA b Q69732-849 corresp sequences may also be used for screen origin of replicat Sequence 48 BP;	9/c 9/c 2694 27-F 10NA 10NA 10NA 10NA	30000000000000000000000000000000000000
14980-A. 101-1993; EC-1993; EC-1993; EP-1993; EP		N N N N N N N N N N N N N N N N N N N
WO9414980-A. 07-JUL-1994; U12388. 20-DEC-1993; US-996783. 21-DEC-1993; US-996783. 23-DEC-1993; US-996783. 23-DEC-1993; US-996783. 23-DEC-1993; US-996783. 26(GENE-) GENELABS TECHNOLOGIES: Andrews BM, Cantor CR, Edwark WPI; 94-234711/28. Sequence-directed DNA-binding r pharmaceuticals and as molecula Claim 28; Page 291; 587pp; Engl A DNA protein-binding assay is libraries of synthetic or bioli to bind DNA test sequences. In number of test sequences can be adjacent to a defined protein- of mols to these test sequence is disturbed, generating change one application fof this method factors (e.g. TFIID), where the from DNA sequences adjacent to transcription factor. Numerous the sequences in 069251-731 and (typically, TATA box-contg. si 069732-849 correspond to promot sequences may also be randomly be used for screening purposes, origin of replication and UL9 i sequence 48 BP; 12 A;	DNA rst for ing ing atio	000000000000000000000000000000000000000
Jagasa. TECHNOLOGIES TOTORIOLOGIES TOTORIOLO	, 48 BP. entry) entry) H4 histone assay; tes TA box; He n; UL9; tr	5444444444 20000000000000000000000000000
is CA, Fry KE is	ALIGNMENTS p. tone, target region. test sequence; screening; Herpes Simplex Virus; H ; transcription factor; T	V70586 Q86183 Q86183 Q86183 T30807 T30807 T35073 T35073 V42384 V42384 V42384 V70704 Q33621
useful in useful in for their ability versatile in that any placing the test sequence placing sequence. Binding the binding characteristics for the DNA, protein complexes mocentration of free DNA probe. yotic general transcription fon is typically selected fite for the eucaryotic test sequences are given: respond to promoter targets an genes and the sequences in for viral genes. The test DNA, protein interaction may lerpes Simplex Virus (HSV) 52, 069865 and 069891).	. ng sequence; . HSV; . TFIID: ds.	Primer 4B used to Primer SINXball700 Primer SINXball700 Sindbis PCR primer Sindbis PCR primer Sindbis-based, tum Sindbis-based, tum Reverse PCR primer Reverse PCR primer Reverse PCR primer Reverse PCR primer Reverse PCR primer Reverse PCR primer

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RESULT 3
X17159/c
ID X17159 standard; DNA; 48 BP
AC X17159;
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CC The sequences given in T63713-4312 represent duplex DNA's which act CC as target regions in the method of the invention. The method for a starget regions in the method of the invention. The method for CC altering the binding characteristics of a DNA-binding protein to duplex DNA with a small molecule which the sequence-specifically to a target region, where, when the small CC binds sequence-specifically to a target region, where, when the small CC molecule is bound to the target region, it is adjacent to, but not concerning by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the concerning by more than 4 bp, a binding site for a DNA-binding site on the duplex DNA. The binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding protein to its binding site. The CC compounds isolated using this method are potentially useful as therapeutic agents for treatment of any disease which involves a generation of sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical CC The method is suitable for screening large biological or chemical CC affinities of known DNA-binding agents for different DNA sequences. CC The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific, or preferential, DNA binding DNA control of the control of the
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Best Local S
Matches 48
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US5869241-A.
09-FEB-1999.
07-JUN-1995.
20-DEC-1993.
27-JUN-1991.
27-JUN-1991.
17-SEP-1993.
U7-JUN-1995.
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US5578444-A.
26-NOV-1996.
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27-JUN-1991; US-723618.
27-JUN-1991; US-723618.
23-DEC-1992; US-996783.
17-SEP-1993; US-172396.
20-DEC-1993; US-172396.
20-DEC-1993; US-172389.
20-DEC-1993; US-172389.
Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
MPI; 97-020402/02.
WPI; 97-020402/02.
Black Cantor CR, Edwards CA, Fry KE, Turin LM;
WPI; 97-020402/02.
Black CA, Fry KE, Turin LM;
WPI; 97-020402/02.
DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer protein's binding site, useful in treatment of viral disease, cancer
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Human H4/a gene (for Histone H4) TFIID binding site.
Human H4/a gene (for Histone H4) TFIID binding site.
Duplex DNA; target region; binding characteristic; DNA binding protein;
TFIID; transcription factor; binding site; inhibition; enhance;
cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
                                                                                                                                                                                                                                                         Test sequence from human H4/a gene for H4 histone.
Test sequence; DNA-binding molecule; screening sequence; human
nucleic acid amplification; target; viral; ds.
     Andrews
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1-1995; 475228.

1-1993; US-171399.

1-1993; US-723618.

1-1992; US-996783.

1-1993; US-123936.

1-1995; US-475228.

1-1995; US-475228.

S BM, Cantor CR, Edwards CA, F.
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Similarity 100.0%;
48; Conservative
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''Asmatches 0;
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     Fry KE,
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     Turin LM
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protectionation of DNA sequence preference of a DNA-hinding molecule - based on inhibition of estinding of protein to oligonic decide probable on inhibition of estinding of protein to oligonic decide probable of the inhibition of estinding of protein to oligonic decide protein of continuous distribution of estinding protein to oligonic decide protein and an analysis of the invention of determining the Sequences X17001 to X17500 represent specifically claimed target test combanguage preference of a bay-hinding malecule. The method compless of the sequence of the sequence of the method compless of the combanguage of the invention of determining the combanguage of the invention of determining the combanguage of the sequence of the test sequence of the protein of test sequence of the protein of the test molecule to test sequence of the protein of the test molecule to test sequence of the protein of test sequences and the sequence of the protein of the protein
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PT Claim 6; Column 185-186; 264pp; English.

CC The sequences given in T63713-4312 represent duplex DNA's which act CC asterget regions in the method of the invention. The method for CC altering the binding characteristics of a DNA-binding protein to duplex CC DNA comprises contacting the duplex DNA with a small molecule which CC DNA comprises contacting the duplex DNA with a small molecule which CC binds sequence-specifically to a target region, where, when the small cc molecule is bound to the target region, it is adjacent to, but not converlapping by more than 4 bp, a binding site for a DNA-binding protein. CC The small molecule is added at a concentration effective to alter the contact converlapping of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding of the small molecule may inhibit or enhance compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as specific DNA sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical contact the second of these duplex DNA's allows a single DNA:protein DNA binding sequences. The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific, or preferential, DNA binding the contact of the design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific, or preferential, DNA binding the contact of the sequence almost any possible sequence (see also T49539-
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Matches 47
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Matches 47
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27-JUN-1991; 723618.
27-JUN-1991; US-723618.
27-JUN-1991; US-996783.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
20-DEC-1993; US-171389.
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                                       12078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-1997 (first entry)
14-MAR-1997 (first entry)
Human H3 histone gene TFIID binding site.
Buplex DNA; target region; binding characteristic; DNA binding protein;
TFIID; transcription factor; binding site; inhibition; enhance; hCG;
cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrews BM, Cantor CR, WPI; 97-020402/02.
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US5578444-A.
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                                                                                                                                                                               Sequence
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CAATAGTTGGTGGTCTGACTCTATAAAAGAAGAGTAGCTCTTTCCTT
                    CAATAGTTGGTGGTCTGACTCTATAAAAGAAGAGTAGCTCTTTCCTT 12124
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l Similarity 100.0%;
47; Conservative 0;
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47; Conserv
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                                                                           Score 47; DB 1; L
Pred. No. 0.00018;
0; Mismatches 0;
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ID 107
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Best Local Similarity
"-+ches 47; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PT Determination of DNA sequence preference of a DNA-binding molecule - PT based on inhibition of binding of protein to oligonucleotide PT sequence attached to test sequence Claim 3; Columns 187-188; 270pp; English.

CC Sequences X17001 to X17600 represent specifically claimed target test columns sequence of a DNA-binding molecule. The method comprises:

CC DNA sequence preference of a DNA-binding protein to a mixture of couls and a DNA-binding protein to a mixture of couls and a DNA-binding protein to a mixture of couls and a DNA-binding protein with a binding screening sequence adjacent to a screening sequence, where the construction of the DNA-binding protein with a binding can affinity that is independent of the DNA-binding protein with a binding considered that the mixture of duplex DNA sequence of the test sequence, cand where the mixture of duplex DNA test oligonucleotides includes several test sequences; (ii) incubating the test molecule, the mixture of duplex DNA test oligonucleotides includes several test sequences; (ii) incubating the test molecule, the mixture of coligonucleotides and the DNA-binding protein for a time coligonucleotides bound to binding protein; (iv) amplifying the unbound test oligonucleotides from test coligonucleotides; (v) repeating steps (ii) to test sequences in the amplified test oligonucleotides; and (vi) sequencing the isolated test oligonucleotides. Test sequences and test sequences X17482-X17599 correspond to promoter targets for viral genes.

Sequence 47 BP; 13 A; 8 C; 10 G; 16 T;
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09-FEB-1999; 475228.

07-JUN-1995; US-171389.

20-DEC-1999; US-171389.

27-JUN-1991; US-723618.

23-DEC-1992; US-996783.

17-SEP-1999; US-475228.

07-JUN-1995; US-475228.

(GENE-) GENELABS TECHNOLOGIES INC.

Andrews BM, Cantor CR, Edwards CA, F.

WPI; 99-152755/13.
WO9414980-A.
07-UUL-1994.
20-DEC-1993; U12388.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
(GENE-) GENELABS TECHNOLOGIES I
ANDREWS BM, CANTOR CR, EDWARD
WPI; 94-234711/28.
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Test sequence; DNA-binding molecule; scree nucleic acid amplification; target; viral;
                                                                                                                                                                                                                                                                                                                                                                       promoter; target; TATA origin of replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human H2a histone g
DNA protein-binding
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llarity 100.0%
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histone H3 gene.
ng molecule; screening sequence;
``~~~**: viral; ds.
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                                               OGIES INC.
Edwards C
                                                                                                                                                                                                                                                                                                                                                                       test sequence; screening sequence; Herpes Simplex Virus; HSV; transcription factor; TFIID: ds.
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RESULT
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PS Claim 28; Page 295; 587pp; English.
CC laim 28; Page 295; 587pp; English.
CC librarles of synthetic or biological cycle. for their ability
CC librarles of synthetic or biological cycle. for their ability
CC number of test sequences. The assay is versatile in that any
CC number of test sequences can be tested by placing the test sequence
CC adjacent to a defined protein-binding screening sequence. Binding
CC of mols to these test sequences changes the binding characteristics
CC of the protein mol not its cognate binding sequence. When such a mol
CC of the protein mol not its cognate binding sequence. When such a mol
CC of the protein of this method is to encaryotic general transcription
CC one application of this method is to encaryotic general transcription
CC factors (e.g. TFIID), where the target region is typically selected
CC transcription factor. Numerous exemplary test sequences are given:
CC the sequences in 069251-731 and 069850 correspond to promoter targets
CC (typically, TATA box-conty, sites) for human genes and the sequences in
CC sequences may also be randomly generated. DNA:protein interaction may
CC origin of replication and UJ9 (see 050851-52, 069865 and 069891).
SQ Sequence 46 BP; 10 A; US (Se 050851-52, 069865 and 069891).
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The sequences given in T63713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for altering the binding characteristics of a DNA-binding protein to duplex DNA comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small molecule is bound to the target region, it is adjacent to, but not overlapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding of the small molecule may inhibit or enhance the binding of the DNA-binding protein to its binding site. The compounds isolated using this method are potentially useful as therapeutic agents for treatment of any disease which involves a specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1991; 723618.
27-JUN-1991; VS-723618.
27-JUN-1991; US-723618.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
17-SEP-1993; US-123936.
20-DEC-1993; US-171389.
(GENELABS TECHNOLOGIES INC.
Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
MPI; 97-020402/02.
MPI; 97-020402/02.
Altering binding characteristics of DNA binding proteins to duplex
DNA - by attaching specific small cpd. to target region close to the
DNA - by attaching specific small cpd. to target region close to the
DNA - by attaching specific small cpd. to target region close to the
DNA - by attaching specific small cpd. to target region close to the
DNA - by attaching site, useful in treatment of viral disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human H2a histone gene TFIID binding site.

Duplex DNA; target region; binding characteristic; DNA binding protein;

TFIID; transcription factor; binding site; inhibition; enhance; hCG;

cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
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US5578444-A.
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ilarity 100.0%;
Conservative
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Matches Query Match Best Local :

Local

ch 0.2%; l Similarity 100.0%; 46; Conservative

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Mismatches

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Length 46;

Qy . 10562 CACAGCCTACCTCCAGTCAGTATAAATACTTCTCTGCCTTGCGTTC 10607

1 CACAGCCTACCTCCAGTCAGTATAAATACTTCTCTGCCTTGCGTTC

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PT Determination of DNA sequence preference of a DNA-binding molecule - PT based on inhibition of binding of protein to oligonucleotide PT sequence attached to test sequence PT sequence attached to test sequence PT sequences X17001 to X17600 represent specifically claimed target test CC sequences X17001 to X17600 represent specifically claimed target test CC sequences X17001 to X17600 represent specifically claimed target test CC sequences that are used in the method of the invention of determining the CC INA sequence preference of a DNA-binding molecule. The method comprises: CC (1) adding a test endecule and a DNA-binding protein to a mixture of duplex DNA test oligonucleotides, each of the test oligonucleotides CC affinity that is independent of the DNA sequence of the test sequence, where the mixture of duplex DNA test oligonucleotides includes and where the mixture of duplex DNA test oligonucleotides includes and where the mixture of duplex DNA; (iii) separating who test molecule to test sequences in CC sufficient to permit binding of the test molecule, the mixture of oligonucleotides bound test oligonucleotides from test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the suplified test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the abolated test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the solated test oligonucleotides; (v) rest sequences X17001-X17481 and X17600 correspond to promoter targets for viral genes.

Sequence 46 BP; 10 A; 16 C; 6 G; 14 T;
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Best Local S
Matches 46
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07-JUN-1995; 475228.

20-DEC-1993; US-171389.

27-JUN-1991; US-723618.

27-JUN-1991; US-966783.

17-SEP-1993; US-475228.

07-JUN-1995; US-475228.

(GENE-) GENELABS TECHNOLOGIES INC.

ANDREWS BM, CANTOX CR, Edwards CA, FI

WPI; 99-152755/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10562 CACAGCCTACCTCCAGTCAGTATAAATACTTCTCTCTGCCTTGCGTTC 10607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences. The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also T49539-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-1999 (first entry)
Test sequence from human histone H2a gene.
Test sequence; DNA-binding molecule; screening sequence; human; nucleic acid amplification; target; viral; ds.
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X17167;
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Pred. No.
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G;
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RESULT
T63881
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DAC PRESENTATION OF PRESENTATI
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PS Claim 28; Page 296; 587pp; English.

CC A DNA protein-binding assay is provided, useful for screening

CC libraries of synthetic or biological cpds. for their ability

CC to bind DNA test sequences. The assay is versatile in that any

CC number of test sequences can be tested by placing the test sequence

CC adjacent to a defined protein-binding screening sequence. Binding

CC of mols. to these test sequences changes the binding characteristics

CC of the protein mol. to its cognate binding sequence. When such a mol.

CC of the protein mol. to its cognate binding sequence. When such a mol.

CC of the protein mol. to its cognate binding sequence. When such a mol.

CC is disturbed, generating changes in the concentration of free DNA probe.

CC is disturbed, generating changes in the concentration of free DNA probe.

CC one application of this method is to eucaryotic general transcription

CC factors (e.g. TFIID), where the target region is typically selected

CC transcription factor. Numerous exemplary test sequences are given:

CC the sequences adjacent to the binding site for the eucaryotic

CC transcription factor. Numerous exemplary test sequences are given:

CC transcription factor. Numerous exemplary test sequences are given:

CC transcription factor. Numerous exemplary test sequences are given:

CC transcription factor. Numerous exemplary test sequences are given:

CC transcription factor. Numerous exemplary test sequences are given:

CC transcription factor of the binding site for the eucaryotic

CC transcription factor. Numerous exemplary test sequences are given:

CC transcription factor. Numerous exemplary test sequences are given:

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CC transcription factor. Numerous exemplary test sequences in the sequences in the sequences of the sequences in the sequences of the sequences in the sequences.

CC of the protein mol. to the protein transcription and UD (see 059851-52, 069855 and 069891
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Best Local Similarity
Matches 45; Conser
              26-NOV-1996.
27-JUN-1991; 723618.
27-JUN-1991; US-723618.
27-DEC-1992; US-996783.
17-SEP-1993; US-123936.
20-DEC-1993; US-123936.
20-DEC-1993; US-171389.
(GENE-) GENELABS TECHNOLOGIES INC.
ANDROWS BM. CANTOR CR. Edwards CF.
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23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
(GENE-) GENELABS TECHNOLOGIES INC.
(GENE-) Cantor CR, Edwards CA,
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Human H3 histone gene, target region.
Human H3 histone gene, target region.
DNA protein-binding assay; test sequence; screening sequence;
promoter; target; TATA box; Herpes Simplex Virus; HSV;
origin of replication; UL9; transcription factor; TFIID: ds.
                                                                                                                                                                                                                                                                                                                        US5578444-A.
                                                                                                                                                                                                                                                                                                                                                                            Human H3 histone gene TFIID binding site.

Buplex DNA; target region; binding characteristic; DNA binding protein;

TFIID; transcription factor; binding site; inhibition; enhance; hCG;

cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA; 45
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Determination of DNA sequence preference of a DNA-binding molecule -
property based on inhibition of binding of protein to oligonucleotide
process of inhibition of binding of protein to oligonucleotide
process of the sequence
process of the sequence of a DNA-binding molecule. The method comprises:
Claim 3; Columns 185-186; 270pp; English.
Sequences X17001 to X17600 represent specifically claimed target test
sequences x17001 to X17600 represent specifically claimed target test
Claim 3; Columns 185-186; 270pp; English
Sequences X17001 to X17600 represent specifically claimed target test
claim 3; Columns 185-186; 270pp; English
Sequences x17001 to X17600 represent specifically claimed target test
Claim 3; Columns 185-186; 270pp; English
Claim 3; Columns 185-186; 270pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1999.

07-JUN-1995; 475228.

20-DEC-1993; US-171389.

27-JUN-1991; US-723618.

27-JUN-1991; US-956783.

17-SEP-1993; US-475228.

(GENE-) GENELABS TECHNOLOGIES INC.

ANDREWS BM, CANTOT CR, EDWARDS CA, FY

WPI; 99-152755/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Test sequence from human histone H3 gene.
Test sequence; DNA-binding molecule; screening sequence; human; nucleic acid amplification; target; viral; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
US5869241-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that recognise almost any
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0.00065;
0;
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RESULT 13
Q62216; standard; DNA; 30 BP.
Q62216; standard; DNA; 30 BP.
AC Q62216; provide #1.
AC Q62216; provide #1.
D7 22.NOV-1994 (first entry)
D8 Histone H3 mRNA probe #1.
KW diagnosis; cancer; carcinogen;
QS Synthetic.
PN W09408046-A.
QP 109408046-A.
PP 109408046-A.
PP 20-CST-1993; G91977.
PR 02-CCT-1992; GB-020777.
PR 02-CCT-1993; G91977.
PR 02-
RESULT 1
Q62217/c
ID 2017/c
ID 22-N
DT 22-N
DE Hist
KW Probl
KW Synt
PN W094
PD 114-p
PF 20-S
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150 - SEP-1993; G01977.

161 - APP 1994.

171 - APP 1994.

172 - CT-1992; GB-020777.

173 - APP 1994.

174 - APP 1994.

175 - APP 1994.

175 - APP 1994.

176 - APP 1994.

176 - APP 1994.

176 - APP 1994.

177 - APP 1994.

178 - APP 1994.

179 - APP 1994.

170 - AP
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Best Local &
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12518 CGAGTGACTATTATGCCCAAAGACATCCAG 12547
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                                                                                                    22-NOV-1994 (first entry)
Histone H3 mRNA probe #2.
Probe; histone; H2b; H3; H4; mRNA;
diagnosis; cancer; carcinogen; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sufficient to permit binding of the test molecule to test sequences in the duplex DNA; (iii) separating unbound test oligonucleotides from test oligonucleotides bound to binding protein; (iv) amplifying the unbound test oligonucleotides; (v) repeating steps (i) to (iv); (vi) isolating the amplified test oligonucleotides; and (vii) sequencing the isolated test oligonucleotides. Test sequences x17001-x17481 and x17600 correspond to promoter targets for human genes and test sequences x17482-x17599 correspond to promoter targets for rural genes.

Sequence 45 BP; 8 A; 6 C; 10 G; 21 T;
                                                                                                                                                                                                                                                                                                     Q62217 standard; DNA;
Q62217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WÖ9408046-A.
14-APR-1994.
20-SEP-1993; G01977
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; Pred. No. 0.00065;
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                                                                                                                                                                                       detection; proliferation; cell;
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9;
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RESCRIPTION OF THE PROPERTY OF
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밁
                                                                                                                                                                                                                                                               Detecting proliferating cells in tissue or cell samples - by probes specific for histone manh for radioactively labelled oligonuclectide probes specific for histone manh for the sequences given in 062216-18 are probes which are specific for histone H3 mRNA. These probes may be used in the method of the invention for detecting the presence of proliferating cells in a converted for the succession of the method comprises preparing the tissue/cell cample. The method comprises preparing the tissue/cell cample, hybridising these non-radioactively labelled probes, and detecting the presence of histone-probe hybrids. The method can be used to identify cells undergoing proliferation in normal and diseased tissue. It can be used in the diagnosis of cancers and in assessing the carainogenic properties of a chemical.

Sequence 30 BP; 4 A; 6 C; 9 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      problem in the method control in the method can be problem specific for histone many be used in the method of the invention H3 manyle. These problem may be used in the method of the invention for detecting the presence of proless may be used in the method of the invention for detecting the presence of proliferating cells in a constant, cells ample. The method comprises preparing the tissue/cell sample, hybridising these non-radioactively labelled probes, and detecting the presence of histone-probe hybrids. The method can be used to identify cells undergoing proliferation in normal and diseased tissue. It can be used in the diagnosis of cancers and in assessing the carainogenic properties of a chemical.

Seguence 30 BP; 7 A; 7 C; 8 G; 8 T;
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Best Local Similarity
                                                                                                                          Matches
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Best Local
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20-SEP-1993; G01977.
02-OCT-1992; GB-020777.
(UYLE-) UNIV LEICESTER.
Pringle JH;
WPI: 94-135606/16.
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                                  12177 GTACTAAACAGACAGCTCGGAAATCCACCG 12206
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Probe; histone; H2b; H3; H4; mRNA; detection; proliferation; cell;
diagnosis; cancer; carcinogen; ss.
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Q62218
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(UYLE-) UNIV LEICESTER.
Pringle JH;
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30 GTACTAAACAGACAGCTCGGAAATCCACCG
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                                                                                                                                                      Similarity
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                                                                                                                      Conservative
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                                                                                                                                                  0.1%;
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                                                                                                                                                  Score 30;
Pred. No.
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Pred. No.
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9;
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80
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/cgn2_6/ptodata/1/lna/5C_COMB.seq:*
/cgn2_6/ptodata/1/lna/5C_COMB.seq:*
/cgn2_6/ptodata/1/lna/6_COMB.seq:*
/cgn2_6/ptodata/1/lna/backfiles1.seq:*
/cgn2_6/ptodata/1/lna/backfiles1.seq:*
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US-08-450-673C-69
US-08-450-673C-57
US-08-450-673C-57
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US-08-475-228A-159
US-08-123-936-159
US-08-171-389-159
US-08-171-389-170
US-08-171-389-167
US-08-171-389-167
US-08-171-389-167
US-08-475-228A-167
US-08-475-228A-169
US-08-171-389-169
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US-08-454-557C-69
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                                                                   Matches
                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                              APPLICATION UMBER: US/08/454,557C
APPLICATION: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.384000:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                               TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
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                                                                   Similarity 58; Conserv
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US-08-859-998-318
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US-08-454-557C-67
US-08-450-673C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-450-673C-91
US-08-659-721-5
US-08-659-721-5
US-08-659-721-5
US-08-450-673C-91
US-08-557C-91
US-08-557C-91
US-08-557C-91
US-08-360-725-5
                                                                   Score 58; DB;
; Pred. No. 2.10
0; Mismatches
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Sequence 318, App
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 92, Appl
Sequence 92, Appl
Sequence 92, Appl
Sequence 93, Appl
Sequence 91, Appl
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RESULT 2
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US-08-450-673C-69
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Best Local S
Matches 58
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ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIOM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIOM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/340,426D

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: LIGHTY, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/POCKET NUMBER: 0609.3840002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEPHONE: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5948634
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 69, Application US/08450673C Patent No. 5948888
                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
APPLICANT: wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2685 GCCCCGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTTCACCGTGTTTGGCCAGGATG 2742
                                                                            COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                      STREET: 1100 New CITY: Washington STATE: D.C.
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CITY: Washington
STATE: D.C.
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1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202) 371-2540
OR SEQ ID NO:
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TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                   NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE_DOCKET NUMBER: 0609
TELLECOMMUNICATION INFORMATION:
TELLEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 69, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
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Best Local Similarity 100.0%; Pred. No. 2.1e-0;
Matches 58; Conservative 0; Mismatches 0;
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: PCT/US95/17111A
APPLICATION NUMBER: PCT/US95/17111A
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APPLICATION NUMBER: 08/340,426
FILING DATE: 14.NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITILE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                               LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.C.
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1100 New York Avenue, Suite 600
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US-08-340-426D-57
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; Sequence 57, Ap
                                                             Sequence 57, Application US/08340426D Patent No. 5948634
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2685 GCCCCGCTAATTITTGTATTTTTAGTAGAGAGAGAGGGTTTCACCGTGTTGGCCAGGATG 2742
                                                                                                                                                                                                                                       2685 GCCCCGCTAATTTTTGTATTTTTAGTAGAGAGACAGGGTTTCACCGTGTTGGCCAGG 2739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
            TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/454,557C FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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                                                                                                                                                                                                                          GCCCCGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGG
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                60 base pairs
                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                            0,
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Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                            Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                            DB 3;
. 2e-09;
                                                                                                                                                                                                                                                                                                                            Length 60;
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                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                        Gaps
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 57, Application US/08450673C Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08-450-673C-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/340
ETILING DATE: 14-NOV-1994
CLASSIETICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwidy, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TET FEINOME: 7,701 471-2600
          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwid, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de la Monte,
APPLICANT: Wands, Jack
                                                                                                                APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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20005-3934
                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                              D.C.
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                                                                                                                                                                                                                                                                                                                              3: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, Suite 600
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202)
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                                0609.3840004
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5. 2e-09;
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US-08-450-673C-57
  RESULT 9
US-08-171-389-159/c
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PCT-US95-17111A-57
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                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base ~ '-'
Type.
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                                                                                                                                                     Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 60 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION :
REFERENCE/DOCKET UNMEER: 36,203
REFERENCE/DOCKET UNMEER: 0609.3840002
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2685 GCCCCGCTAATTTTGTATTTTAGTAGAACAGGGTTTCACCGTGTTGGCCAGG 2739
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/34
FILING DATE: 14 NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                   Local Similarity
es 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20005-3934
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                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                   both
                                                                                                                                                     0.2%; Score 55; DB 6; Length 60; 100.0%; Pred. No. 2e-09; tive 0; Mismatches 0; Indels
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                                                                                                                                                   Indels
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US-08-123-936-159/c
US-08-123-936-159/c
; Sequence 159, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
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; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO : ORIGINAL SOURCE: INDIVIDUAL ISOLATE: Human H4/a gene for H4 histone US-08-171-389-159
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
APPLICATION NUMBER: US 07/723,618
APPLICATION NUMBER: US 07/723,618
APPLICATION NUMBER: US 08/081,070
PRIOR APPLICATION NUMBER: US 08/081,070
PRIOR DATE: 22-JUN-1991
PRIOR DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
BEGITEPRATTON WIMPER: 33.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 159, Application US/08171389 Patent No. 5578444
                                                                             Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fig. Kirk E.

TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94063
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Cantor, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                          0.2%; Score 48; DB 1; ilarity 100.0%; Pred. No. 4.1e-07 Conservative 0; Mismatches 0
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Charles R.
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                                                                                                                  Length 48;
                                                                               Indels
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; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
US-08-123-936-159
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US-08-475-228A-159/c
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                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                     Sequence
                                                                                                                      GENERAL INFORMATION:
APPLICANT: Edward
APPLICANT: Cantor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 324-09 TELEFAX: (415) 324-096 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
APPLICATION NUMBER: 27-JUN 1991
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                 22582 GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCTGCCCCC 22629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                           APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequences: 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
              CORRESPONDENCE ADDRESS
                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fablan, Gary R. REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                               GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCTGCCCCC 1
                                                                                                                                                                    59, Application US/08475228A
5869241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                       Edwards, Cynthia A Cantor, Charles R.
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                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                          Andrews, Beth M.
Turin, Lisa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Genelabs Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening Assay for the Detection of DNA-Binding Molecules
                             Sequence-Directed DNA Binding Molecules, Compositions and Methods 664
                                                                                                                                                                                                                                                                                                                                           0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human H4/a gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/123,936
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                                                                                                                                                                                                                                                                                                                                           Score 48; pred. No.
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                           4.1e-07
                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                       H4 histone
                                                                                                                                                                                                                                                                                                                                                          Length 48
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                                                                                                                                                                                                                                                                                                                            0
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US-08-475-228A-159
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US-08-482-080A-159/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                         APPLICANT: Turi:
APPLICANT: Fry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                             ADDRESSEE:
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                 CA
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Sequence 159, Application US/08482080A Patent No. 6010849
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                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/475,2284
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
                                            TITLE OF INVENTION: Sequence-Directed DNA Binding TITLE OF INVENTION: Molecules, Compositions and M NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
                                                                                                                                            APPLICANT: Edwards, Cynthia A. APPLICANT: Cantor, Charles R. APPLICANT: Andrews, Beth M.
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LENGTH: 48 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,4
Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
             E: Genelabs Technologies, Inc
505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 base pairs
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                                                                                                             n, Lisa M.
Kirk E.
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                                                                                                                                                                                                                                                                                                                                                                                           0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human H4/a gene for H4 histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/996,783
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Pred. No.
                                                                              Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 13
PCT-US93-12388-159/c
; Sequence 159, Application PC/TUS9312388
; GENERAL INFORMATION:
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FILLING DATE: 17-SEP-1993
PRIOR APPLICATION UNMBER: US 07/996,783
FILLING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/996,783
FILLING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILLING DATE: 27-UN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILLING DATE: 22-UN-1993
ATTORNET/AGENT INFORMATION:
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.2
REGISTRATION INFORMATION:
TELEPONNE: (650) 324-0860
INFORMATION SED ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.2%; Score 48; DB 5; Best Local Similarity 100.0%; Pred. No. 4.1e-07 Matches 48; Conservative 0; Mismatches 0
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-UUN-1995
PRIOR APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
BORITON TON DATA:
IN OR APPLICATION DATA:
IN OR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                             TITLE OF INVENTION: Sequence-Directed DNA Binding TITLE OF INVENTION: Molecules, Compositions and Methods NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
TRATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: UN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCCTGCCCCC 1
                                                                                                                      COUNTRY: UZIP: 94063
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                                                                                                                                            USA
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REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 4600-0175.41/G19PCT2
REFERENCE_DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
GOTATION: 1502
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US-08-171-389-170
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PCT-US93-12388-159
                                                                                                                                                                           APPLICANT: Turin, Lisa M.

APPLICANT: Ery, Kirk E.

APPLICANT: Ery, Kirk E.

APPLICANT: Ery, Kirk E.

TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 641

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTUMARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
NEDITALIZATION DATA:
NEDITALIZATION MITMARED: NECKNISTION #1.25
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Best Local Similarity
Matches 48; Conserv
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Patent No. 5578444
GENERAL INFORMATION:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 23-DEC-1992
ATTORNEY_AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DN
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PRIOR APPLICATION DATA:
APPLICATION UDATA:
US 08
APPLICATION UDMBER: US 08
FILING DATE: 17-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Edwards, Cynthia A. APPLICANT: Cantor, Charles R. APPLICANT: Andrews, Beth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
ORIGINAL SOURCE:
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23-DEC-1992
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Gaps

FILING DATE: 23-DEC-1992 PRIOR APPLICATION DATA:

US 07/723,618

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US-08-123-936-170
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Best Local Similarity 100.0%;
Matches 47; Conservative 0
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LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC COMPATIBLE
COMPUTER: PS COMPATIBLE
COMPUTER: PS COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKEY NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                APPLICATION NUMBER: US 07/723,618 FILING DATE: 27-JUN 1991 ATTORNEY/AGENT INFORMATION:
                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Edwards, Cynthia A
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Screening Assay for the Detection TITLE OF INVENTION: DNA-Binding Molecules
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 505 Penopse
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 94063
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAATAGTTGGTGGTCTGACTCTATAAAAGAAGAGTAGCTCTTTCCTT 47
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505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08123936
                                                                                                                                                                                                                                                                                                                                                                    USA
                  Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cynthia A.
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8.8e-07;
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Search completed: March 30, 2000, 17:28:35 Job time: 135577 sec
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                                                                                                                                                                                                            ; INDIVIDUAL ISOLATE: US-08-123-936-170
                                                                                                                                  Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 170:
                                                                       MOLECULE TYPE: DN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                               0.2%; Score 47; DB 2; L
100.0%; Pred. No. 8.8e-07;
                                                                                                                                                                                                                             Human histone H3 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                4600-0075.32/G19P2
                                                                                                                                    0;
                                                                                                                                      Mismatches
                                                                                                                                                               Length 47;
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                                                                                                                                    Gaps
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Page 8

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Minimum DB seq length: 8
Maximum DB seq length: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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30001
1 TGGCCAGCTGCAGGTGGCGGG.....TATTCTAAGCCATGGTCAAT 30001
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13816.393 Million cell updates/sec
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em_est8:*
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em_est5:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 1	Result
53	ult Query No. Score Match Length DB ID
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98 31	ength DB
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c 1 53 0.2 98 31 AA280198 AA280198 zt04b12.r	Description

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AA280198/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Fumor Gene Index Tumor Gene Index Unpublished (1997) Unpublished (1997) On Sep 12, 1996 this sequence version replaced ya... Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LNL; contact the This clone is available royalty-free through LNL; contact the This clone is available royalty-free through LNL; contact the This clone is available royalty-free through LNL; contact the This clone is available royalty-free through the This clone royalty-free through the This clone royalty royalty-free throu
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98 bp mRNA EST 14-AUG-1997 zt04b12.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:71.2127 5/ similar to contains Alu repetitive element; contains element MER22. repetitive element; mRNA sequence.

AA280198

AA280198.1 GI:1921755
EST.
                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 98)
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National Cancer Institute, Cancer Genome Anatomy
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D48914
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AIB61185 tc79h04.x
AAB09831 coA40f11.s
AAB09831 coA70f0.s
AAB132822 at72909.s
AAB132822 at72909.s
AAB14379 np46c03.s
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AAB170104 tc277002.x
AAB28120 co271301.s
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AAB12997 za66h04.r
AAB12997 za66h04.r
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AA457423 aa86b02.r
A1932967 w040f09.x
AQ626158 CITBI-E1-
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1 (bases 1 to 70)

1 (bases 1 to 70)

1 (chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Lacy, M., Le, M., Le, N., Karlis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
53; Conserv
                                                                      High qality sequence stops: 54
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
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IMAGE:79815
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The vector to vector length is 99
Insert Length: 622 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham.
Location/Qualifiers
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97044478
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                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                     Email: est@watson.wustl.edu
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ilarity 100.0%;
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//Clone_ILb="NCI_CGAP_GCB1"
//Lisue_type="germinal center B cell"
//Lb_host="DHIOB"
//Lb_host="DHI
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/db_xref="taxon:9606"
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repetitive
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                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 102)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ319270 102 bp DNA GSS 06-MAY-1999 RPCI-11-98B22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-98B22,
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Other_GSSs: RPCI11-98B22.TV
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AQ319270
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Location/Qualifiers
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/db_xref="GDB:7537293"
/db_xref="taxon:9606"
/clone="RPCI-11-98B22"
                                                                  /sex="Male"
                                                                                                                                                                                                                 Location/Qualifiers
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/clone="IMAGE:79815"
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'note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                      clone_lib="RPCI-11"
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                                           cell_type="Lymphocytes"
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Best Local Similarity
Matches 43; Conserv
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                                     1283 GGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAA 1325
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24 GGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAA
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nes 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)

Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavici Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABI Chromatograms and other information are available on WWW http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Via Trieste 75, 35121 Padua,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Pad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRIBI Biotechnology Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Valle G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Apr 7, 1998 this sequence version
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                                                                         Conservative
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                                                                                                                                                                                      ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beats. ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector." a 19 c 38 g 16 t
                                                                                                                                                                                                                                                                                                  /tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a blotinylated
oligo-dT-NotI primer
(5'-blotin-AACCCGGCTTGAGCGGCCGCTTTTTTTTTTTTTTTTT-3'). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000074G04"
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Pred. No. 4.1e-05;
0; Mismatches 0;
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RESULT 5 AA457423/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 92)

1 (NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NALIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index.
                                                                                                                                                                                                                                                                                                      A1932967 92 bp mRNA EST 02-SEP-1999 wo40f09.xl NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457833 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
On Nov 4, 1996 this
Contact: Wilson RK
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Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1134104.
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AI932967.1 GI:5671704
                                                                                                                                                                                                                                                                                    mRNA sequence.
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This clone is available roya
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//note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled
retinal tissue. Average insert size: 1.0 kb; Uni-ZAP XR
Vector: -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"

adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"

25 g 17 t
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/db_xref-"taxon:9606"
/clone-"IMAGE:838155"
/clone_lib-"Stratagene fetal retina 937202"
/sex-"mixed"
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M., Martin,J.,
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                                                                   Email: bbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                Unpublished (1997)
Other_GSS8: CITBI-21-2650p18.TF
CONTACT: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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GSS.
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CITBI-E1-2650P18.TR CITBI-E1
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 104)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.69 kb. Life Technologies catalog
11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
/db_xref="taxon:9666"
/clone="Indage:2457833"
/clone=llb-"NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host-"DH10B"
       1. .104
/organism="Homo sapiens"
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16-JUN-1999 clone 2650P18,

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Best Local
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Best Local Similarity
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Local Similarity 100.0%;
nes 41; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 52)

Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K. Global analysis of gene expression in colon mucosa: a large scale random cDNA sequencing analysis

Unpublished (1994)

Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K Institute for Molecular and Cellular Biology

Osaka University

Jramada-oka, Suita, Osaka 565, Japan.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                          B48914.1 GI:2601151 GSS.
                                                                                                                 B48914 103 bp DNA RPCI11-4A12.TP RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D25879.1 GI:500543
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMGS05672 Human colon mucosa Homo sapiens cDNA clone cm2335 3',
                                                                                       B48914
                                                                                                   genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                 0.1%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                               /clone="cm2335"
/clone_lib="Human colon mucosa"
/note="Adult male, tissue_type =
17 c 14 g 9 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1;
CalTech Human BAC Library D"
28 c 22 g 42 t
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="2650P18"
/clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                              Score 40; DB 20;
; Pred. No. 0.0031;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Pred. No.
                                                                                                                   sapiens
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0.00098;
ches 0;
                                                                                                               GSS
genomic
                                                                                                                                                                                                                                                                                             Length 52;
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                                                                                                                                                                                                                                                                                                                                                                        colon mucosa
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                                                                                                                   clone
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KEYWORDS
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AUTHORS
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VERSION
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AI864984/c
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Best Local S
Matches 40
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          wk06cll.xl
similar to
                    Unpublished (1997)

On May 18, 1998 this sequence version replaced gi:3137794.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11547-015

DNA Sequencing by: Washington University Genome Sequencin
Clone distribution: NCI-CGAP clone distribution informati
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter, J.C.
Use of BAC End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 103)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                      Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
28 c 30 g 15 t
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1. .103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:7501163"
/db_xref="taxon:9606"
/clone="RPCI-11-4A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 bp mRNA EST 30-AUG-1999 NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2411540 3' contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 GI:5529091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 103;
                                          Sequencing (information
                                                                                                                                                                                                                                        Project (CGAP),
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                                            n can be
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primer:

-40UP from Gibco

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REFERENCE
AUTHORS
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AI801185/c
LOCUS
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VERSION
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Best Local S
Matches 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
On Mar 16, 1998 this sequence version replaced gi:2961671.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
AI801185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI801185 05-UTL-1999 06-UTL-1999 to79h04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184535 3' similar to gbi M87921|HUMALCD120 Human carcinoma cell-derived Alu RNA transcript, (rRNA); contains element TAR1 repetitive element;
                                                                                                                                                                                                                                                                       Seg primer: -400P from Gibco High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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37; Conservative
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                                                                          /Clone_"IMAGE:2184533"
/Clone_1ib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-*Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
a 29 c 27 g 21 t
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone='IMAGE:2411540"
/clone_lib="MCI_CGAP_Lym12"
/tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No.
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0.025;
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AUTHORS
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AA809831/c
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  Query Match
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Local Similarity 100.0%; P
mes 35; Conservative 0;
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ca40f11.s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2287025.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 963 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 60.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., D
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases.1 to 88)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA809831.1
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                                                                                                                                                                                                                              /note="vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc Ri; Ist strand create prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+ IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
                                                                                 /tissue_type="germinal center B cell"
/tab_host="bell0B"
/note="vorter" =
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1307469"
/clone_lib="NCI_CGAP_G(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 bp mRNA EST 19-FEB-1998 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307469 contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:2879237
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  Score
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  Length 88;
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ibution information can b
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JOURNAL COMMENT
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                                                                       Query Match
Best Local :
                                                         Matches
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            3853 CCCGCCTCCGCCTCCCAAAGTGCTGGGATTACAGG 3887
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 CCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1093
High quality sequence stops: 65
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1093 Std Error: 0.00
Seq primer: Promega -21m13
User Description (1880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 96)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R67088 96 bp mRNA EST 30-MAY y130h05.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140793 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Apr 5, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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R67088.1 GI:839726
                                                                     Similarity
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Conservative 0;
                                                                                                                                              25
                                                         Conservative
                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                    100.0%;
                                                                                    0.18;
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                                                                    Score 35; DB 22;
Pred. No. 0.12;
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; Mismatches
                                                        Mismatches
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AQ535244/c
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 ORGANISM
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Best Local
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35; Conserv
Homo sapiens
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18986 GTGAAACCCCGTCTCTACTAAAAAAAAAAAAAAAA 19020
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AQ535244 103 bp DNA GSS 18-RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-317H22, genomic survey sequence.
AQ535244
AQ535244 GI:4846934
GSS.
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Inpublished (1997)
On Mar 20, 1998 this sequence version replaced gi:2980211.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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AI591270
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1 (bases 1 to 102)
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.1%; Score 35; DB 48; Length 102: llarity 100.0%; Pred. No. 0.12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DHIOB"
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/note="Organ: bone marrow; Vector: pAMP1; mRNA made from
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myelogenous leukemia"
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/db_xref="taxon:9606"
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AUTHORS
Search completed: March 30, 2000, 13:20:07 Job time: 122661 sec
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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E 1 (bases 1 to 103)

S Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (lifo@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                           31
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/cell_type="Lymphocytes"
/note="Vector: pBAC63.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 27 c 27 g 18 t
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1. .103
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Title: Perfect score: Sequence:

Scoring table:

OLIGO_NUC , Gapop 60.0 ,

Run 용

nucleic 9

Minimum

Word size Searched:

Maximum

DB DB

seq length: 8 seq length: 105

Post-processing: Listing first

gb_pat:*
gb_ph:*
gb_pl1:*
gb_pl2:* gb_pr1:*

gb_pr3:* gb_pr2:* 35_om: *

em_hum1:*
em_hum2:*

gb_un : * gb_sy:* gb_ro:*

em_or:*
em_ov:* em_in:*
em_om:*

em_ro:*

gb_htg1: *
gb_htg2: *
gb_in1: *
gb_in2: *
em_ba1: *

em_vi:* em_un:* em_sy:* em_sts:* em_pl:* em_ph:* em_pat:*

gb_pr4:* gb_htg3:* gb_htg4:* gb_htg5:*

GI:5974851

em_hum3:*
em_hum4:*

em_ba2:*

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Db 16 TTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTT 53
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                                                                                                                                                                           HUMALUANCD 67 bp DNA PRI (Homo sapiens 4000 year old remains from Nekht-ankh fragment 12:5.
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Sequence 69 from patent US 5830670.
AR051499
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1 (bases 1 to 60)

1 (bases 1, 5, and Wands, J.R.

Neural thread protein gene expression and detection of Alzheimer's disease
Ancient DNA: extraction, characterization, molecular cloning, and enzymatic amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: US 5830670-A 69 03-NOV-1998; Location/Qualifiers
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de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's
                                                                                       Homo sapiens
                                                                                                    Homo sapiens (individual_isolate 4000 year old remains from
Nekht-ankh) liver DNA.
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission

Submitted (21-UTL-1993) to the DDBJ/EMBL/GenBank databases. Ryo

Matoba, Osaka University, Institute for Molecular and Cellular Bio;

Matoba, Osaka University, Institute for Molecular and Cellular Bio;

(E-mail:matoba@inherit.imcb.osaka-u.ac.jp,

Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)

2 (bases 1 to 51)

Matoba, R., Okubo, K., Hori, N., Fukushima, A. and Matsubara, K.

The addition of 5'-coding information to a 3'-directed cDNA library

dene 146 (2), 199-207 (1994)

94357437
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89184542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene signature.
Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMD6B03M3 51 bp mRNA PRI Human HepG2 3' region MboI cDNA, clone hmd6b03m3.
                                                                                                                                                                                                                                                                                                                                                                            Ryo Matoba
Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology for the Earth 9-2
Kizugawadai Kizu-cyo,
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D17279.1 GI:598922
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Primates; Catarrhini; Hominidae; Homo.
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07747-5-2321
                                                                                             /organism="Homo sapiens"
/db_xef="taxon:9606"
/cell_line="Hep62"
/clone_lib="Kiseru"
/sex="Male" 12 g 7
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/isolate="4000 year old re
/db_xref="taxon:9606"
/tissue_type="liver"
<1. >67
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35; Conservative 0;
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Submitted (30-MAR-1995) James L. Weber, Medical Genetics,
Marshfield Medical Research Foundation, 1000 N. Oak Ave.,
Marshfield, WI 54449, USA
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1 (bases 1 to 79)

Arcot, S.S., Wang, Z., Weber, J.L., Deininger, P.L. and Batzer, M.A. Alu repeats: a source for the genesis of primate microsatellites Genomics 29 (1), 136-144 (1995)
                                                                                                                                                                                                                                                                                                                                                                                  AF087511 66 bp mRNA
Homo Sapiens clone ENaC+22 epithelial
(SCNNIA) mRNA, alternatively spliced,
AF087511
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Batzer,M.A., Rubin,C.M., Hellmann-Blumberg,U., Alegria-Hartman,M.,
Leeflang,E.P., Stern,J.D., Bazan,H.A., Shaikh,T.H., Deininger,P.L.
and Schmid,C.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hylobates sp. sequence homologous to Human dinucleotide repeat region clone Mfdl58, sequence tagged site.
                                                            An Alu cassette in the human 
Unpublished
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 65)
Oh,Y. and Warnock,D.G.
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      와, Y.
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(bases 1 to 66)
Y. and Warnock, D.G
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/db_xref="taxon:9581"
/chromosome="7"
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Pred. No. 6.7e-06;
0; Mismatches 0;
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Submitted (26-AUG-1998) Medicine,
Birmingham, AL 35294, USA
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                                                       33; Conserv
                                                                                                                                                                                                                                                                 GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 155288] from the original journal article. This sequence comes from Fig. 3a.
                                                                                                                                                                                                                                                                                                                          Canaani,E., Bloomfield,C.D. and Croce,C.M.
ALL-1 tandem duplication in acute myeloid leukemia with a normal karyotype involves homologous recombination between Alu elements Cancer Res. 54 (16), 4277-4280 (1994)
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1 (bases 1 to 79)
Schichman, S.A., Caligiuri, M.A., Strout, M.P., Carter, S.L., Gu,
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/note="alternatively spliced epithelial sodium channel alpha subunit containing intronic Alu sequence"
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/db_xref="taxon:9606"
/chromosome="12"
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RESULT 8 HUMBRKFAA/c

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32; Conser
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80)
1 (bases 1, bishop, D.F. and Desnick, R.J.
Kornreich, R., Bishop, D.F. and Desnick, R.J.
Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
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Human alpha-galactosidase breakpoint family F.
M36132
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1 (Dases 1 to 80)

1 (Dases 1 to 80)

1 (Dases 1 to 80)

1 (Nornreich, R., Bishop, D.F. and Desnick, R.J.

1 Alpha-galactosidase A gene rearrangements causing Fabry disease: Identification of short direct repeats at breakpoints in an
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Human alpha-galactosidase breakpoint region.
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ilarity 100.0%; Pred. No. 0.00021;
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les 31; Conservative
                                                 2 (bases 1 to 76)
2 (bases 1 to 76)
2ietkiewicz,E., Richer,C., Sinnett,D. and Labuda,D.
2ietkiewicz,E., Richer,C., Sinnett
   Canada Sequences corresponding to the PCR primers used to amplify
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Primates; Strepsirhini; Galagonidae; Ocolemur.
1 (bases 1 to 76)
2 letklewicz, E., Richer, C., Sinnett, and Labuda, D.
Monophyletic origin of Alu elements in primates
7. Mol. Evol. 47 (2), 172-182 (1998)
                                                                                                                                                                                                                                                                                                                                                                                              thick-tailed bush baby. Otolemur crassicaudatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF032238 76 bp
Otolemur crassicaudatus
AF032238
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Direct Submission
Submitted (20-AUG-1998) Hematology, Erasmus University Rotterdam, Dr. Molewaterplein 50, Rotterdam 3015 GE, The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van der Reijden,B.A., Dauwerse,H.G., Giles,R.H.,
Jagmohan-Changur,S. and Breuning,M.H.
Nonoverlapping genomic inv(16)(p139.22) CBFB intron 5 breakpoint
regions ordered centromeric to telomeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF032238.1 GI:2642069
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AF084969.1 GI:3659831
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1 (bases 1 to 60)
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/db_xref="taxon:9606"
/chromosome="16"
/map="16922"
a 20 c 15 g 12
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100.0%; Pred. No. 0.00066;
tive 0; Mismatches 0;
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clone GALII27 Galago Alu.
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                                                                                               /note="deletion target
19 a 34 c 25 g
Chromosome 19p13.2-p13.1.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            h 0.1%; So Similarity 100.0%; 31; Conservative 0;
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Location/Qualifiers
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/clone="GALII27"
                                                                                                                                                                                  /gene-"LDLR"
/note-"LDLR intron
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20 c 21 g
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join(M14178.1:1. .97,1.
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HUMLDLRDJ/c
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1 (bases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
J. Mol. Biol. (1992) The press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="deletion target sequence" 22 a 34 c 23 g 18 t Chromosome 19p13.2-p13.1.
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Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hobbs,H.H., Brown,M.S., Goldstein,J.L. and Russell,D.W. Deletion of exon encoding cysteine-rich repeat of low density lipoprotein receptor alters its binding specificity in a subject with familial hypercholesterolemia
J. Biol. Chem. 261, 13114-13120 (1986)
                                                                                                                                                                                                                                                                                            Homo sapiens
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Alu repeat.
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1 (bases 1 to 97)
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/db_xref="taxon:9606"
42...72
              /tissue_type="carcinoma"
27 c 33 g 1
                                                /dev_stage="embryo"
/sex="male"
                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
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Db 12 GCCCACCTTGGCCTCCCAAAGTGCTGGGAT 41
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Human alpha-galactosidase breakpoint region.
M36131
M36131.1 GI:179541
Fabry disease; breakpoint junction; glycosphingolipid catabolism.
Human DNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 80)
Kornreich, R., Bishop, D.F. and Desnick, R.J.
Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                                                                                                                                                                                                Alu-rich gene
J. Biol. Chem. 265, 9319-9326 (1990)
90264427
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/db_xref-"taxon:9606"
19 a 28 c 20 g 13 t
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12258.117 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Reverse PCP
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Microsatellite ana
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Reverse PCR primer
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Homo sapiens clone
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RESULT TO4081/c ID TO4081/c ID TO408 AC TO408 AC TIYP KW TIYP KW TIYP KW TIYP KW TIYP KW TO722 AC AC A POC CC Or 1

Trypsin inhibitory protein cDNA antisense primer-1.
Trypsin; inhibitor; human T98G cells; pancreatitis; shock; DIC; multiple organ failure; disseminated intravascular coagulation;

88

16-MAY-1996 (first entry) 04081 standard; DNA; 48

BP

s Synthetic.

y 707242700-A.

y 107242700-A.

D 19-SEP-1995.

p 04-MAR-1994; 059906.

y 04-MAR-1994; 0

treatment

22-28 kD

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Qγ	X B O	PT P			00000 000 00
29696 AA	Query Match Best Local Matches 2	SCHOOL MEDICINE. SCHOOL MEDICINE. Gelman IH, Lauren WPI; 94-026200/03. HIV-LP useful in w distinct from HIV- Example; page 7; 7 HIV-LP is a new vas synthesised from P converted into dsD primers Q55167 and Sequence 40 BP;			& & & & & & & & & & & & & & & & & & &
AAAAA	Simi 8;		standard; 1994 (fi. 2e of prim. .mmunodefi. .i.c. .1923. .1993. .1993. .1993. .1993. .1993. .1993.		222335555555
AAAAAAAAAAAAAAAAAAAAAAA	h Similarity 28; Conserva	CONNECTION PROPERTY OF THE PRO	9/C 8/C 955168 standard; DNA; 40 BP. 955168; 21-JUL-1994 (first entry) 22-JUL-1994 (first entry) Sequence of primer for PCR am Human immunodeficiency virus; Synthetic. 909400562-A. 06-JAN-1994. 06-JAN-1994. 06-JAN-1994. 106-JAN-1993; U06162. 24-JUN-1993; U05162. 24-JUN-1992; US-903421. 19ORNELL RES FOUND INC		000000000000
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29723	Score 28; DB 1; Length Pred. No. 16; 0; Mismatches 0; Inde	mulations - is novel HIV IV-2 viruses sh. The HIV family. A CDNA fire t using MLV RT. The produst CDNA was amplified by Fred. No. 16; Score 28; DB 1; Length Pred. No. 16; Street No. 16; Mismatches 0; Ind	plification of HIV-LP Pt. HIV-LP; PCR primer; ss.	ALIGNMENTS	V15487 T28941 V12343 V03013 V03013 T95781 T9523 Q93960 T39266 T39266 T39288 V39388 V39388 V39388 V39388
	40; }1s 0;	virus st strand lot was CR using	1 isolate		PR-1 promoter pr naChr beta2 subu Ribonucleotide r Aspergillus oryz Repeat sequence Template switch! Intronic human w Primer RI-Not-T Primer MBTA from PCR suppression PCR suppression Primer of the sp EP-892047 Seq II
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RESULT
Q95177
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Matches 28
                                                                                                                                                                                                                                                                                                                                                                          A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of the 7837 "GS" sequences or in T19001-T28837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-or of mRNA by using poly(T) as the sole primer. Since the 3'-outranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency off a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognishing different cell types.
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11-NOV-1996 (first entry)

Human gene signature HUMGS07164.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

Homo sapiens.

MO9514772-A1.

101-NOV-1993, JD-355504.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsubara K, Okubo K;
MPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
Q95177 standard; DNA; 57 BP
Q95177;
08-FEB-1996 (first entry)
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Oy 16309 GCCCAGGCTGGAGTGCAGTGGCGTGATC 16336
24-APR 1997:

1906; U16637.

PR 19-0CT-1995; U5-005598.

PR WPI; 97-245107/22.

PR WPI; 9
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21-DEC-1994; G02789.
21-DEC-1994; G02789.
21-DEC-1993; GB-026052.
21-DEC-1994; GB-026052.
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Claim 26; Page 17; 51pp; English.

Q95177 is a simple tandem repeat (STR) corresponding to the 2nd part

of wgla2. The STR can be used for treatment and diagnosis in human
and veterinary medicine, partic. for genetic characterisation,

mapping, linkage studies and analysis/diagnosis of acquired disease

alleles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                second part; ss.
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W09517522-A2.
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Synthetic.
W09714790-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB; Pred. No. 15
0; Mismatches
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15;
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Similarity

0.1%; ilarity 100.0%; Conservative

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Score 28; DB Pred. No. 15; 0; Mismatches

DB 1;

Length 60

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RESULT
X00174/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requence - capable of forming ligatable hairpin structured promoter and transcribing target sequence, is sensitive and useful in medical diagnosis?

The sequence 1; 15pp; English.

The sequence is an example of a preferred T7 RNA polymerase promoter for use in the invention. There can be from 2 to 50 T's in the loop region. A probe sequence is ligated to the 3' end of the promoter region. Upon hybridisation of the probe to a target sequence and ligation of the hybridisation of the probe to a target sequence hairpin-forming sequence, the target sequence can be transcribed by T7 RNA polymerase. This allows the target sequence to be amplified (and detected) using a single oligonucleotide component (c.f. PCR). See also Q11759 and Q11761-Q11764.

See also Q11759 and Q1761-Q11764.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP-427073-A.
15-MAY-1991.
27-OCT-1990; 120650.
09-NOV-1989; US-434372.
23-AUG-1990; US-569991.
                                                                                                                                                                                                                                                                                                                                                                                                29692
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Self-complementary, T7 promoter hairpin-forming
T7 bacteriophage; DNA-dependent RNA polymerase;
                                                                                                                                    10-DEC-1998.
05-JUN-1998; U12141.
05-JUN-1997; US-048662.
                                                    New recombinant porcine reproductive and respiratory syndrome virus - containing nucleic acid encoding a polymerase from an RNA virus and open reading frames 2-7 of the porcine virus, used particularly
                                                                                                                                                                                                                                 Porcine reproductive and respiratory syndrome virus PCR primer PRRSV-2. Equine arteritis virus; EAV; vaccine; structural gene; PRRSV; porcine reproductive and respiratory syndrome virus; recombinant virus.
                                                                                                                                                                                                                                                                                                   X00174 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid probe for amplification and detection of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dattagupta N;
WPI; 91-141638/20
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 The present inve
polymerase from
                                                                                             Coussens PM, Reilly JD, WPI; 99-080829/07.
                                                                                                                                                                              WO9855626-A2.
                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                   PCR primer; ss.
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                             Example 2; Page
                                                                                                                         (ORIG-) ORIGEN INC.
                                                                                                                                                                                          Porcine reproductive
                                                                                                                                                                                                                                                                                           X00174;
                                           in vaccines
                                                                                                                                                                                                                                                                          3-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                    Similarity 100
28; Conservative
 invention de from an RNA
                             21;
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/*tag=
/note=
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                                                                                                                                                                                                                                                                                                      DNA;
                             55pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0.1%;
describes a nucleic acid which encodes
A virus, excluding porcine reproductive
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"number of T's
                                                                                                           Spatz
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                                                                                                                                                                                                                                                                                                      ΒP
                                                                                                                                                                                           respiratory syndrome virus
                             English.
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Pred.
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VIEW PRESCRIPTION OF THE P
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                                                                                                                                                                                                   RESULT
T23178
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of yeast artificial chromosomes by in vivo recombination using vector comprising yeast centromere, marker, recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination

Stample 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the All repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                             15-JAN-1998.
09-JUL-1996; U11478.
09-JUL-1996; WO-U11478.
(USSH ) US DEPT HEALTH & HU
KOUPTINA NY, LATIONOV VL, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1998 (first en., )
28-JUL-1998 (first en., )
Alu PCR primer 1.
PCR; primer; amplification; Alu repeat sequence; vector;
PCR; primer; amplification; Alu repeat sequence; vector;
30-AUG-1996 (first entry)
Human gene signature HUMGS04920.
Gene signature; messenger RNA; mRNA;
human; cloning; mapping; non-biased l
cell typing; abnormal cell function;
                                                                                                                                            T23178
T23178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory syndrome virus (PRRSV), and open reading frames (ORFs) 2-7 of PRRSV. The use of a polymerase gene from RNA viruses can provide for production of less mutagenic recombinant viruses. The recombinant viruses can be used in vaccines which have a reduced risk of loss or reduction of efficacy. The vaccines are used particularly for protecting swine against PRRSV. The high fidelity RNA polymerase gene can be used as a marker that allows organisms vaccinated with such a vaccine to be distinguished from organisms naturally infected with wild type strains of virus or other vaccines. The present sequence represents a PCR primer used in an example from the present invention.

Sequence 98 BP; 11 A; 14 C; 8 G; 65 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces sp
WO9801573-A1.
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                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                           27;
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28; Conservative
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VL, Perkins EL, Resnick MA;
                                                                                                                                                                         mRNA;
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Pred. No. 13;
0; Mismatches
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Pred. No.
                                                                                                                                                                         61
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                                                                                                                                                                         ВP
                               library;
                                                            relative abundance;
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                                  diagnosis;
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                                  detection;
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DNA can
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RESULT 1
V37197/c
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PS Example 1; Page 44; 68pp; Japanese.
CC The present sequence is used in the course of the invention. The Specification describes a molecule for bringing together genotype with CC phenotype (in vitro virus). The molecule contains a nucleic acid contains a nucleic acid prenotype vortein fragment containing a protein participating in CC fragment having a base sequence corresponding to a genotype, covalently condition to a protein part via a puromycin modely. The nucleic cold fragment preferably consists of RNA corresponding to the gene (free CC acid fragment preferably consists of RNA corresponding to the gene (free CC adapter (such as a DNA-TRNA hybrid containing an anticodon corresponding to the terminator codon), a spacer (such as two-stranded DNA), a peptide containing and a puromycin-containing cap containing cap to the terminator codon of the gene) and a puromycin-containing cap capable of binding to an amino acid residue. Translation of the virus is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences of as a means of diagnosing abnormal cell function or for sequences as a means of diagnosing abnormal cell function or for Sequence 61 BP; 23 A; 12 C; 14 G; 12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18097 GATCACGCCACTGCATTCCAGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K
MPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                                (MITU ) MITSUBISHI CHEM CORP.
Fusimi Y, Miyamoto E, Nemoto N, Yanagawa H;
WPI; 98-261039/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-1998 (first entry)
01igonucleotide sequence of the specification.
one of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genotype; phenotype; molecular ev
functional biopolymer; virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1305; 2245pp; Japanese. A single-stranded DNA (or its complem
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1998.
17-OCT-1997; J03766.
17-OCT-1996; JP-274855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GATCACGCCACTGCATTCCAGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.1%;
| Similarity 100.0%;
| 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okubo K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Query Match Best Local S Matches 27

Similarity 27; Conser

0.1%;

Score 27; DB ;; Pred. No. 26; 0; Mismatches

DB 1; 26;

Length 88;

0,

0

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V 3597044

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PT Sequencing nucleic acid by mass spectrometric analysis - for detecting nucleic acids, telomerase activity, oncogene mutations, or pr detecting nucleic sequences, for diagnosis of disease ps Example 1; Page 318; 478pp; English.

CC A process has been developed for determining the sequence of a target cucleic acid. The process comprises: (1) generating at least two creaments (F) from the target nucleic acid; and (1) analysing F by comess spectrometry (MS). The sequences in V39483 to V39592 are specifically claimed primers for use in the mass spectrometric analysis co f the above process. The process is used to detect genetic diseases cofficially claimed primers for use in the mass spectrometric analysis coffices, cystic fibrosis and many others) or chromosomal abnormalities comparisition; infections and cancers; also for establishing cidentity and heredity. Particular applications are diagnosis of neuroblastoma, detecting telomerase, determining family relationships can disposition; this process requires fewer specific reagents can is better suited to automation. Extended primers are shorter; cand is better suited to automation. Extended primers are shorter; colligonucleotide used in an example from the present invention.

Sequence 88 BP; 56 A; 5 C; 7 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer specific sequence;

Synthetic,

W09820166-A2.

14-MAY-1998,

06-NOV-1997; U20444.

06-NOV-1996; US-74481.

06-NOV-1996; US-744636.

06-NOV-1996; US-746036.

06-NOV-1996; US-746036.

06-NOV-1996; US-746036.

05-NOV-1996; US-746036.

05-NOV-1996; US-746036.

05-NOV-1996; US-746036.

05-NOV-1996; US-746036.

23-JAN-1997; US-78638.

23-JAN-1997; US-787639.

19-SEP-1997; US-983792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP 1998 (first entry)
Microsatellite analysis antisense strand SEQ ID NO:262.
Mass spectrometry; diagnosis; detection; biological sample;
genetic disease; chromosomal abnormality; identification; he
pathogenic organism; telomerase activity; oncogene mutation;
cancer specific sequence; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           performed in a non-cellular (preferably ribosomal) system (e.g. E. coli ribosome), the protein synthesised by the translation attaching to the puromycin cap, resulting in the complete in vitro virus structure. The method is used in molecular evolutionary engineering to optimise function of a functional biopolymer such as an enzyme, antibody or ribozyme, or to generate new functionality. The virus can be used for the functional optimisation of nucleic acid or protein sequences.

Sequence 80 BP; 7 A; 10 C; 1 G; 62 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SEQU-) SEQUENOM INC.

Braun A, Damboffer-Demar B, Fu D, Higgins GS, Jurinke
Braun A, Little DP, Lough DM, Siegert CW, Tang K,
Koster H, Little DP, Lough DM, Siegert CW, Tang K,
Van Den Boom D, Xiang G;
WPI; 98-286975/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.1%;
ilarity 100.0%;
Conservative (
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pred. No. 27;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
27;
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23274 AAAAATAAATAAATAAATAAATAAATA

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acid sequence (I) in a sample. The method comprises: (a) hybridising (I) to the probe ends of a probe having 2 free nucleic acid end parts, which CC are at least partially complementary to and capable of hybridising to at least 2 neighbouring regions of (I); (b) covalently connecting the cc ends of the hybridised probe with each other to form a circularised contacture; (c) washing under denaturing conditions, characterised in that the probe is provided with a cleavable or dissociable detectable function; (d) cleaving or dissociating the detectable function; (d) cleaving or dissociating the detectable function; (e) separating probes with connected ends from probes with non-connected ends by washing under denaturing conditions; and (f) detecting the presence and, if desired, location of the remaining probe as indicative of the presence of (I). The present sequence represents a padlock probe, can be used to detect, quantify and distinguish between sequence variants with regard to 1 or several (I) in a sample. It can be used to disease, for genetic linkage analysis of biallelic markers and to consist the presence of (I) by allowing a detectable consisted to that it reports the presence of (I) by allowing a detectable consisted to the presence of (I) by allowing a detectable consisted to the probe is designed so that it reports the probe has been cyclised in a target dependent linking reaction. It also provides for high specificity and consisted to background reduction.
 RESULT
Q75099,
ID Q7
AC Q7
DT 11
DE P1
KW Ps
OS HC
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Best Local S
Matches 27
                                                                                                                                                                                                       29696 ААААААААААААААААААААААА
                                                 Q75099 standard; cDNA; 95
Q75099;
11-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1998 (first entry)
Padlock probe alphaFV from WO9741254.
Cleavable padlock probe; target nucleic acid;
circularised structure; hybridisation; Factor
Plasmid pOKSC18a contg. portion of Psychosis protecting protein; PCR; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 7; 20pp; English.
The present invention describes a method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting target nucleic acid sequence - using probe forming circularised structure, which can be cleaved detectable function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1997; SE0737.
30-APR-1996; SE-001676.
(LAND/) LANDEGREN U.
                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jandegren U
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                                                                                                                                                                                                                                                       Similarity
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ilarity 100.0%;
Conservative
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/note= "attached to an amino group"
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                 psychosis
primer; ss
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                                   protecting protein
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V; ss.
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                                                                                                                                                                                                                                                                            Length 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable
to form
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                                                                                                                                                                                                                                          Gaps
                                     gene
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Query Match Best Local S Matches 27

ch 0.1%; S l Similarity 100.0%; 27; Conservative 0;

Score 27; DB Pred. No. 25; 0; Mismatches

DB 25;

0

0

Gaps

0

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Length 100

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RESULT
V68827,
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PD 24-NOV-1994: U05445.

PF 13-MAY-1993; U5-060560.

PR 13-MAY-1993; U5-060560.

PR 13-MAY-1993; US-060560.

PR 13-MAY-1946.

PR 13-MAY-1993; US-060560.

PR 13-MAY-193; US-060560.

PR 13-MAY-193;
DR WPI; 98-557473/47.

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Best Local S
Matches 27
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11-DEC-1997; US-991789.
09-APR-1997; US-838762.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; epitope;
Homo sapiens.
WO9845328-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA molecule encoding a breast tumour specific polypeptide #19 Human; breast cancer; breast tumour tissue; diagnosis; treatme vaccine; epitope; endogenous; retroviral element; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frudakis TN, Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-1999
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l Similarity 100.0%;
27; Conservative (
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74. .95
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1. .28
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SG, Smith
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"see above"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JM;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Page 6

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Post-processing: Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length: 105
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Match
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                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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     Gapext 60
US-08-454-557C-57

US-08-450-673C-57

US-08-450-673C-57

US-08-454-557C-69

US-08-450-673C-69

US-08-450-673C-69

PCT-US95-17111A-69

US-08-233-609-5

US-08-233-609-5

US-08-244-083-5

US-08-244-745-5

US-08-443-129-5

US-08-443-129-5

US-08-443-130-5

PCT-US95-04467-5

US-08-322-766A-3

US-08-322-766A-3

US-08-322-766A-3

US-08-329-164-2

US-08-739-167-21

US-08-739-167-21

US-08-739-167-21

US-08-739-167-21

US-08-739-167-21

US-08-739-167-94

US-08-671-914A-1
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   sequence
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                 57, Appl 59, Appl 69, Appl 69,
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US-08-454-557C-57
Sequence 57, App
Patent No. 58306
                                Q
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                                                                                                                                                   US-08-454-557C-57
                                                                                                                                                             APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUDW19, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: NUCLeic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0000
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                                                                 Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIT: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
TENDET APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein G
TITLE OF INVENTION: of Alzheimer's Disease
UNMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                   1 Similarity
38; Conserv
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ilarity 100.0%;
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US-08-113-646A-39
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US-08-222-177A-349
US-08-378-494B-114
US-08-381-572-20
US-08-381-572-20
US-08-63-823B-72
US-08-653-823B-72
US-08-653-823B-72
US-08-778-494B-111
US-08-778-494B-111
US-08-522-269B-18
US-08-522-269B-18
US-08-522-269B-18
US-08-778-494B-16
US-08-778-494B-67
                                                                                                                                                                                                                                                                                                                        0609.3840003
                                                                                     Score 38; pred. No.
                                                                   0
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                                                                   Mismatches
                                                            ; DB 3; L., do. 0.00064; 0;
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Sequence 39, Appl
Sequence 40, Appl
Sequence 114, App
Sequence 20, Appl
Sequence 20, Appl
Sequence 70, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 111, App
Sequence 111, App
Sequence 111, App
Sequence 111, Appl
Sequence 111, Appl
Sequence 111, Appl
Sequence 111, Appl
Sequence 116, Appl
Sequence 16, Appl
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US-08 450-673C-57

US-08 450-673C-57

; Sequence 57, Application US/08450673C

; Patent No. 594888

; GENERAL INFORMATION:
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; Sequence 57, Application US/08340426D
; Patent No. 5948634
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340
FILING DATE: 14 NOV-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Ludwig, Steven R. 0.3
REGISTRATION NUMBER: 36.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                               APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection ITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TITTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTT 53
                                                                                                                      STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: D.C.
                                                                    ZIP: 20005-3934
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ZIP: 20005-3934
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                                                                                                                                                                      ADDRESSEE:
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38; Conserv
                                                                                                           D.C.
                                                                                                                                               E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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100.0%; Pr
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Pred. No. 0.00064;
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      CT-US95-17111A-57
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57, Application PC/TUS9517111A GENERAL INFORMATION:
                                                                                                                             TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -US95-17111A-57
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                             NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 0609.3840002
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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APPLICANT: Wands, Jack R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 TTTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 20005-3934
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITY: Washington
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EDNESS: both
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                                                                                 60 base pairs
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371-57:
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; Pred. No. 0.00064;
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RESULT 6
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                                                                            Sequence 69, Application US/08340426D Patent No. 5948634
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Best Local
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                    17232 TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTT 17269
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ludwig, Steven R. REGISTATION NUMBER: 36,203
REFERENCE_DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/01
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: de la Monte, :
APPLICANT: Wands, Jack R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITLE OF INVENTION:
                                                                                                                                                                        16
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                                                                                      TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTT 53
                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                            76 base pairs
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                                                                                                                                                                                                                                                                                                                             poth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sterne,
                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 371-2600
02) 371-2540
                                                                                                                                                                                                                             0.1%; but
100.0%; Pr
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kessler, Goldstein & Fox P.L.L.C.
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                                                                                                                                                                                                                                 b; Score 38; DB
b; Pred. No. 0.0
0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                  0.00061;
hes 0;
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US-08-450-673C-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILLING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                            STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                        TRY: U.S.A.
20005-3934
                                                                                                                                                                                                                                                                                                                                               Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                               E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 base pairs
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100.0%; Pred. No.
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                                                             0609.3840004
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                                                                                                                                                                                                    Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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69:

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RESULT 9
US-08-233-609-5/c
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PCT-US95-17111A-69
RCT-US95-17111A
REPUBLIANT ON PC/TUS9517111A
REPUBLIANT ON PORT OF PROPERTY 
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                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 0.1%; Score 38; DB 4; L Best Local Similarity 100.0%; Pred. No. 0.00061; Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: PCT/US95/17111A
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SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET, NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                 .ch 0.1%; Score 38; DB 6; I
il Similarity 100.0%; Pred. No. 0.00061;
38; Conservative 0; Mismatches 0;
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1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                                             o,
                                                                                                                                                         RESULT 10
US-08-44-083-5/c
; Sequence 5, Application US/08444083
; Patent NO. 5571675
; GENERAL INTORNATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: Fing, Kathleen
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OY 29696 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29723
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DEATH PC-DOS/MS-DOS

SOSTWARE: Patin (Genentech)

SOSTWARE: Patin (Genentech)

APLICATION NUMBER: US/08/233,609

FILING DATE: 25-APR-1994

CLASSIFICATION NUMBER: US/08/233,609

FILING DATE: NUMBER: US/08/233,609

FILING DATE: APPLICATION DATA:

APPLICATION NUMBER: 25-APR-1994

CLASSIFICATION NUMBER: 28,616

PRIOR APPLICATION NUMBER: 28,616

REFIERNCY/AGENT NUMBER: 28,616

REGISTRATION NUMBER: 894

TELECOMPUNICATION NUMBER: 894

TELECOMPUNICATION NUMBER: 894

TELECAMPUNICATION STANDARTON:

TELEPAN: 415/925-1896

TELEPAN: 415/925-1896

TELEPAN: 415/925-1896

TELEPAN: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 bases

TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 28; Conservative
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08233609 Patent No. 5534615 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 ААРАЛАРАРАРАРАРАРАРАРАРАРАТ 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE ADDRESS: 6
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
COUNTRY: res res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
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CURRENT APPLICATION DATA

OPERATING SYSTEM: PC-DOS AND SOFTWARE: parts

PC-DOS/MS-DOS

360 Kb floppy disk

ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.1%; Score 28; DB 1; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08286304 Patent No. 5571893
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ETILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: TORCHIA, Timothy E.
REGISTRATION NUMBER: 36,700
REGISTRATION NUMBER: 894P1D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                     ZIP: 94000
COMPUTER READABLE FORM:
COMPUTER TEADABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/286,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29696 AAAAAAAAAAAAAAAAAAAAAAAAAAA 29723
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/233609
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
TUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
APPLICATION NUMBER: US/08/286
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 50 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08 FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                               SSEE: Genentech, Inc.
F: 460 Point San Bruno Blvd
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker, Joffre
Chien, Kenneth
King, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pennica, Diane
                                                                                                                                                                                                                                                                              USA
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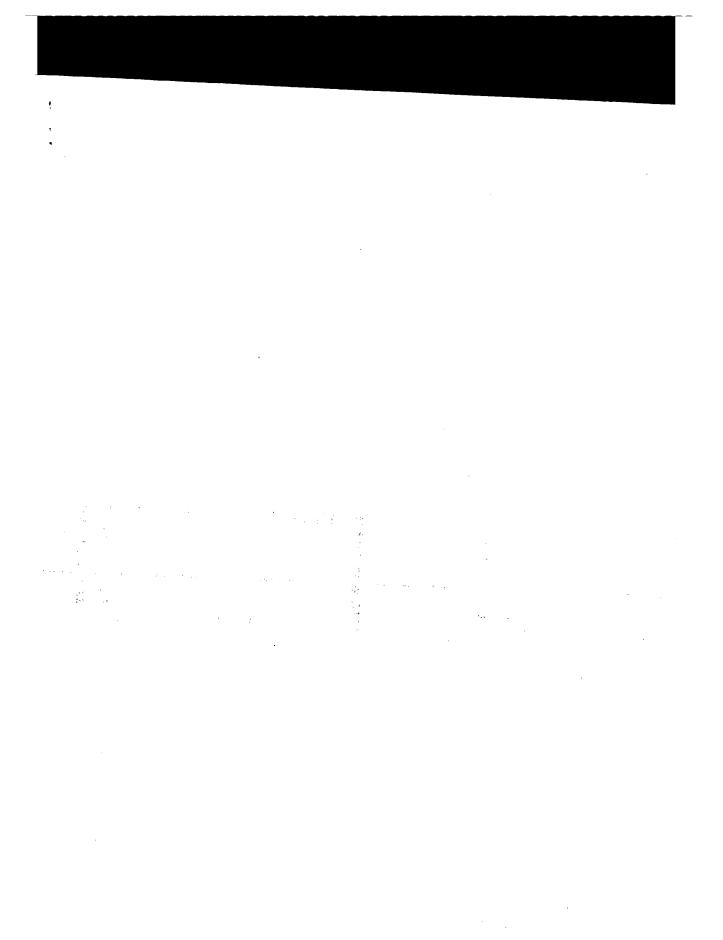
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RESULT 12
US-08-442-745-5/c
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Best Local s
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                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/442,745
FILING DATE: 17-may-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 50 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                   REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: King, Kathleen APPLICANT: Pennica, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baker, Joffre APPLICANT: Chien, Kennet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                    TELEPHONE:
                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 05-AUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                    ELEFAX:
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o. 5624806
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Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   910/371-7168
                                                      910/371-7168
                                                                    415/952-9881
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                                                                                                                                                                                           05-AUG-1994
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                                                                                                                      36,700
R: 894P1D1
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QY 29696 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29723
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
OPERATING SYSTEM: PC.DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,129
EILING DATE: 17-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
APPLICATION NUMBER: 08/286
FILING DATE: 25-APR-1994
APPLICATION NUMBER: 304
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: 304
FILING DATE: (null)
ATTORNEY_AGENT INFORMATION:
NAME: TOTCHA: 36,700
REFERENCE_POCKET NUMBER: 36,700
REFERENCE_POCKET NUMBER: 36,700
REFERENCE_POCKET NUMBER: 36,700
REFERENCE_TOCKET NUMBER: 36,700
REFER
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US-08-443-129-5
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Best Local (
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US-08-443-129-5/c
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TOPOLOGY:
US-08-442-745-5
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 0.1%; Score 28; DB 1; Length 50; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 28; Conservative 0; Mismatches 0; Indels
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APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Renneth
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
COUNTRY. South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 94080
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                                                                                                                                            ch 0.1%; Score 28; DB 1; Length 50; l Similarity 100.0%; Pred. No. 1.3; 28; Conservative 0; Mismatches 0; Indels
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5, 5627073
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MEDIUM TYPE: 3.25 Inch, 360 Kb floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOPTWARE: Patin (Genentech)
APPLICATION UNMBER: US/08/443,952
FILING DATE: 17-MAY-1995
CLASSIFICATION UNMBER: 08/233609
FILING DATE: 17-MAY-1994
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION UNMBER: 08/26304
FILING DATE: 25-APR-1994
PRIOR APPLICATION UNMBER: 08/26304
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1995
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US-08-443-952-5
                                                                                                                                                                                                                      Sequence 5, Application US/08443130 Patent No. 5723585
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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                      GENERAL INFORMATION:
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Patent No. 5679545
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TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Joffre APPLICANT: Chien, Kenneth APPLICANT: King, Kathleen APPLICANT: Pennica, Diane APPLICANT: Wood, William
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 ААААЛААААААААААААААААААА
Baker, Joffre
Chien, Kenneth
King, Kathleen
Pennica, Diane
Wood, William
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TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
ITITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: 460 Point San Francisco
STREE: 460 Point San Francisco
SCREEN SAN FRANCISCO
SCREENTATION BATA: 4029443,130

CLASSITICATION NUMBER: 40233609
FILING DATE: 10 Point San Francisco
STREE: 402 Point San F
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Title:
Perfect score:
Sequence:

Run on:

Scoring table:

Minimum DB Maximum DB

Word size :

Searched:

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13816.022 Million cell updates/sec
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No.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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em_est22 **
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em_est29 **
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JOURNAL
COMMENT
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AUTHORS
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ORGANISM
                                                                                                                                                                                                             ACCESSION
VERSION
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AQ280224/c
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                             Use of a random human BAC End Sequence Databas Map Building
Unpublished (1998)
Other_GSS: CITBI-E1-2522N7.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
                                                                                                              human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Venter,J.C.

Yenter,J.C.
                                                                                                                                                                                                       AQ280224 101 bp DNA GSS 22-NOV-1998 GSS 22-NOV-1998 genomic survey sequence.
                                                                                                                                                                                                   AQ280224.1 GI:3906043
                                                                                                                                                                                                                                                                                                                       a random human BAC End Sequence Database for Sequence-Ready
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39
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36
104
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AAA81256 zs94e09.s
AA655098 nu7dd11.s
B62983 CT-HSP-669
AA807640 nxO8b05.s
AA807640 nxO8b05.s
AA507576 wc02c03.x
A1206568 qr30g11.x
AA501753 ng05a01.s
AA291270 zs18d04.s
T52775 ys79d08.r1
AA564832 n152a06.s
AA835205 ak64h01.s
AA835205 ak64h01.s
AA835205 ak64h01.s
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AA381309 EST94442

AA780764 ac68f12.s

R1780764 ac18610.s

R17033 Yf45406.r2

N80946 za12a02.r1

N80946 za12a02.r1

146088 RPCIII-4N6

AQ541035 RPCI-11-3

AA078003 7H12D08 C

AA07803 7H2D08 C

AA281256 ze94609.s
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AQ319270 RPCII1-98
AA654562 nt75f10.s
AQ584425 RPCI-11-4
AA458985 ZX88h08.s
F26823 HSPD14446 H
AA570476 nk63h12.s
B90619 CITHSP-216
AQ558244 RPCI-11-3
D20898 HMMGSG10-71-3
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T52775 ya79d08.r1
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AUTHORS
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SOURCE
ORGANISM
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AI168167/c
LOCUS
DEFINITION
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Db 70 CAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGT 27
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                                                                                                                                 Eikaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eikaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; CB 1 (bases 1 to 93)

RS NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

RX I-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index
Unpublished (1997)
On Jan 19, 1988 this sequence version replaced g1:2282306.

Enail: Robert Strausberg, Ph.D.

Email: Robert_Strausberg, Ph.D.

Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the Insert Length: 1481 Std Error: 0.00

Insert Length: 1481 Std Error: 0.00

High quality sequence stop: 79.

High quality sequence stop: 79.

Hurce

Location/Qualifiers
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93 bp mRNA

0009e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens CDNA Clone

IMAGE:1565706 3' similar to contains Alu repetitive
element; contains TAR1 repetitive element ;/ mRNA sequence.
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                     AI168167.1 GI:3701337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@ti
  /note-forgan: Pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. a subtractive hybridization, this DNA was used as tracer in pcR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries The pools consisted of the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.1%; Score 44; DB 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
                                                                           Organism="Homo sapiens"

(d)_xref="taxon:9606"

(clone="IMAGE:1565706"

(clone="IMAGE:1565706"

(clone="IDH10B"

(clone_Iib="Soares_NSF_F8_9W_OT_PA_P_S1"

(lab_host="DH10B"

(lab_host="DH10B")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Octl_Type="sperm"
/Octl_Type="sperm"
/Octl="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
28 C 24 g 25 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2522N7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="CITBI-E1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 5,000 clones made from consisted of the following
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Matches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCAGTGAGCCGAAATCGCGCCACTGCACTCCAGCCTGGGT 22481
                                                                                                                                                                                                                                                                                                                          Insert Size: 1013
High qality sequence stops: 82 Source: IMAGE Consortium, clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information. Insert Length: 1013
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasoe,S., Diettich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T52775 95 bp mRNA EST 06-FEB-1995 ya79d08.rl Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:67887 5' similar to contains Alu repetitive element, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95)
                                                                                                                                                                                                                                                                                             High quality sequence stop: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: ya79d08.s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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T52775
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//note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI;
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:504144"
/db_xref="taxon:9606"
/clone="IMAGE:67887"
                                                                                  /dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                  /clone_lib="Stratagene ovary (#937217)"
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0.0027;
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AA837701/c
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25732 AGGAGAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAG 25772
25734 GAGAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAG 25772
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hes 41; Conservative
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AA837701
AA837701.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 17, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 97)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                              h 0.1%;
Similarity 100.0%;
39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ert Length: 451 Std Error: 0.00 primer: -40ml3 fwd. ET from Amers h quality sequence stop: 50. Location/Qualifiers
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                                                                                                                                                                                                      /note="Vector: pampl0; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATTCGGCACGAG 3' ~3' adaptor sequence:
CTCGAGTTTTTTTTTTTTTTTT 3'"
32 c 20 g 24 t
                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1385090"
/clone_11b="NCI_CGAP_Ov2"
                                                                                                                                                                                                                                                                                                          /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovary"
                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 bp mRNA EST 07-APR-1998 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385090 contains element PTR5 repetitive element ; mRNA
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                                                                                  Score 39;
Pred. No.
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; Pred. No.
                                                                                                                                                                                       29
                                                            core 39; DB 39;
Pred. No. 0.024;
Mismatches 0;
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Other_GSSs: RPCIII-98B22.TV
Contact: Shaying Zhao, William Nierman, Mark
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                         AA654562 102 bp mRNA EST 04-NOV-1997 nt75f10.sl NCI_GGAP_pr3 Homo sapiens cDNA clone IMAGE:1204363 similar to contains alu repetitive element;contains element MER22 repetitive element; , mRNA sequence.

AA654562 AA654562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please contact Pieter de Jong library availability, please contact pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from (pleter@dejong.med.buffalo.edu/ordering) or from BACPAC Resources (http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 102)
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RPCI11-98B22.TJ RPCI-11 Homo
                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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301 838 0208
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/db_xref="GDB:7537293"
/db_xref="taxon:9606"
/clone="RPCI-11"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
/note="Vector: pBACe3.5; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
28 c 31 g 17 t
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                                                                                                                     GI:2590716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.1%; Score 39; DB 100; 100.0%; Pred. No. 0.024;
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortim/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 102)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                    AQ584425 103 bp DNA GSS 07-JUN-1999 RPCI-11-458L2.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-458L2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                           Map Bullding
Unpublished (1997)
Other_GSSs: RPCI-11-458L2.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                             Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                    Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 103)
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                         Homo sapiens
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     Contact: Shaying Zhao,
                                                                                                                                              Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
                                                                                                                                                                                                                                                                                                                   AQ584425.1 GI:5011535
                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.18;
Similarity 100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to Ecorl adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

27 g 21 t
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/db_xref="taxon:9606"
/clone="IMAGE:1204363"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Pr3"
/sex="Male"
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        William Nierman, Mark Adams
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0.05;
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SOURCE
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AUTHORS
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1 (bases 1 to 82)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1395423.

Contact: Wilson RK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA458985 82 bp mRNA EST 09-JUN-1997 zx88h08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810879 3' similar to contains LTR5.t2 LTR5 repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA458985
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Seq primer: SP6
Class: BAC ends.
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu/ordezing) or f:
BACPAC Resources (http://bacpac.med.buffalo.edu/ordezing) or f:
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                           IMAGE Consortium (info@image.llnl.gov) for Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 70.
                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                             Washington University School of Medicine
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                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty free through LLNL ; contact the
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Location/Qualifiers
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
27 c 31 g 22 t
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/clone="RPCI-11-458L2"
/clone_lib="RPCI-11"
/organism="Homo sapiens"
/db_xref="GDB:6041714"
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MEDLINE
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1 (bases 1 to 85)

Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.

Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F2682
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On Mar 16, 1998 this sequence version
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HSPD14446 HM3 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Padua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary: Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5' strand cDNA was primed with a Not I oligo(dT) primer [5' double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

27 a 19 c 10 g 26 t
                                                                                                                                                                            /tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
/site_2: NotI; The library was constructed by G.
/site_2: NotI; The library is not subtracted nor normalized.
The first strand cDNA was primed with a blottinylated oligo-dT-NotI primer
/site_1: Distribution of the control of the contro
                                                                      ds cDNA was sonicated and size-selected in the 350-550 bp. The 3' specific fragments were se streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000060G10"
/clone_lib="HM3"
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/clone="IMAGE:810879"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female
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                                               50 TTGGCTCATGCCTGTAATCCCAGTACTTTGGGAGGCC 86
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37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:801194.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: L. J
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Similarity 100.0%;
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theria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 103)
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone=_lib="NACE:1018247"
//clone=_lib="NCI_CGAP_Schl"
//lab_hosf="Schwannoma tumor"
//lab_hosf="Schwannoma tumor"
//lab_hosf="Schwannoma tumor"
//lab_hosf="Schwannoma tumor"
//note="Vector: Bluescript SK-; Site_1: EcoR; Site_2: /note="Vector: Bluescript SK-; Fitmer: Oligo dT. Two pooled bulk Schwannoma tumors. 5' adaptor sequence: 5'
GANTTCGGCACGAG 3' 3' adaptor sequence: 5'
GCCAGGTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.2 kb."
27 a 19 c 31 g 26 t
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100.0%; Pre
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                                                                                                                                               Score 37; DB 35; Length 103; Pred. No. 0.1;
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia; Eutheria: Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 103)
2 hoy.S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cch 0.1%; Score 37; DB 81; Length 103; 1. Similarity 100.0%; Pred. No. 0.1; 1. Similarity 60; Mismatches 0; Indels 37; Conservative 0; Mismatches 0; Indels
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Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
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1 (basia; Ttmates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                            AQ535244 IO3 bp DNA GSS 18
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
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Clones are available from Research Genetics (info@resgen.com). BAC
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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Other_GSSs: CIT-HSP-2163G1.TF
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Seq primer: M13 Reverse
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/sex="Male"
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/clone="2163G1"
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/db_xref="GDB:7100363"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and
after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequencing Unpublished (1993) Contact: Okubo.K., Fukushima.A., Yoshii.J., Niiyama.T., Yoshinari.H., Arimoto.J. and Matsubara.K.
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HUMGS01971 Human promyelocyte
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                            3-1 Yamada-oka,Suita,Osaka 565,Japan.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    Osaka University
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                      Institute for Molecular and Cellular Biology
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Medical Center Dr., Rockville,
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301 838 0208
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promyelocyte.
                                                        /Clone="mp0383"
/clone_lib="Human promyelocyte"
/clone_lib="Adult, cell_line =
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/cell_type="Tymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
27 c 27 g 18 t
                                                 /note="Female, adult,
promyelocyte. "
                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RPCI-11-317H22"
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/db_xref="GDB:7621533"
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This clone is available royalty-free through LLNL; contact the

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Unpublished (1997)
On May 5, 1995 this sequence version replaced
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -28m13 rev1 ET from Amersham
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    Location/Qualifiers
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Insert Length: 758 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
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//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript SK-; Fimer: Oligo dT. Pooled
//note="Twetton: Oligo dT. Pooled retinal tissue. Average insert size: 1.0 kb; Uni-ZAP XR
//note-final tissue. Average insert size: 1.0 kb; Uni-ZAP XR
//note-final tissue. Average insert size: 1.0 kb; Uni-ZAP XR
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 65)

RS Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S.,
Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Inpublished (1997)
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 815-8744
Fax: (206) 815-8744

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B36140
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141125	128514	120514	130350	T23510	A49272	AR051521	AR051440	HUMUT7692A		HOMOTOL	, ,	η 4 Ο	۱ -	HIMALCE272	HUMLDLRA1	HUMLDLRFM	HUMUT6154A	HUMUT6154A	HUMALUANCD	HUMUT243A	•	MGAL	HOMBREAU	HOMBANEAC	HIMBBRENC	100	53	816	HSLAS32	E09140	A25212	U	E22	~	m	S79561	S79560	HUMLDLRDJ	HUMLDLRA2	HUMLDLRM	HUMBRKFAC	AR051499	AR051487	~	A68622	HUMBRKFAB	Ξ	ביים ביים ביים ביים ביים ביים ביים ביים	•	
25 Sequence	.4 sequence	Sequenc	0 00440000	Sections	12 Sequence	521	440	9	16 G.gallus ge	Human STS	ozy mulian sis	Of Cr. All	604 61-4-54-54-	9 Human Caro	78 Human	3556 Human low d	742 Human STS	742 Human	L36843 Homo sapien	93	hibit	23 Huma	135 Huma	135 Human	CLOS Grandi	S Himan alaba	Human	30244 Human STS	1547 H.sapiens D	E09140 Synthetic	inter-Alu	32655 A009I	87896 Human carc	17279 Human Hep	l Sequence 1	<pre>51 dHRX {part</pre>	_	9 Human fami	0 Human	5365 Human	3 Human alp	1499 Sequenc	87 Sequence	55 Human low	8622 Sequence	6132 Human al	136131 Human alp	Description		

ALIGNMENTS

SULT 1		
MBRKFAA/c		
CUS	HUMBRKFAA 80 bp DNA I	PRI 27-APR-1993
FINITION	Human alpha-galactosidase breakpoint region.	lon.
CESSION	M36131	
RSION	M36131.1 GI:179541	

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JOURNAL
MEDLINE
FEATURES
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Db 60 GTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGG 17
                                                                                                      RESULT
A68622/c
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ORGANISM
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                                                                                                                        w
unidentified
                                                          Sequence 2 from Patent W09801573
A68622
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80)
Kornreich,R., Bishop,D.F. and Desnick,R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human alpha-galactosidase breakpoint family F. M36132
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Kornreich, R., Bishop, D.F. and Desnick, R.J.

Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
                                           A68622.1 GI:4759649
                                                                                         A68622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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J. Biol. Chem. 265, 9319-9326 (1990)
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              unidentified
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               h 0.1%; Score 42; DB 9; L Similarity 100.0%; Pred. No. 2.7e-09; 42; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 0.1%; Score 44; DB 9; L
Similarity 100.0%; Pred. No. 2.8e-10;
44; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
1: 28 c 20 g 1:
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/db_xref="taxon:9606"
29 c 16 g 18
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HUMLDLRFL/c
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            Unclassified
                                           Unknown.
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(bases 1 to 60)
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QY 28376 CCGCCTCCCGGGTTCAAGCGATTCTCCTGCCTGAGCCTCC 28415
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sequence 57 from patent US 5830670.
AR051487
AR051487.1 GI:5974851
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Chromosome 19p13.2-p13.1.
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1 (bases 1 to 40)

1 (bases 1 to 40)

Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and Perkins, E.L.

TRANSFORMATION ASSOCIATED RECOMBINATION CLONING

PATENT: WO 9801573-A 15-JAN-1998;

US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alu-Alu recombination in a subject with familial hypercholesterolemia Cell 48 (5), 827-835 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMLDLRFL 90 bp DNA PRI 11-JAN-19
Human low density lipoprotein receptor intron A Alu repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alu repeat; low density lipoprotein receptor-1; repeat region.
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Similarity 100.0%; Pred. No. 2.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                   /gene="LDLR"
/note="hgml; G00-119-362"
/note="hgml; G00-119-362"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p13.3"
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8 c 19 g
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100.0%; Pred. No. 8.2e-08;
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                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 80)

Kornreich, R., Bishop, D.F. and Desnick, R.J.

Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                           Human alpha-galactosidase M36133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR051499 76 bp
Sequence 69 from patent
AR051499
AR051499.1 GI:5974863
                                                                                                                                                          Homo sapiens
                                                                                                                                                                        Fabry disease;
Human DNA.
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Neural thread protein gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neural thread protein gene expression
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                                                                       Alu-rich
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Similarity 100.0%;
38; Conservative (
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ilarity 100.0%;
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                                  Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="unknown"
19 c 18 g
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14 c 15 g
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                                                           265, 9319-9326 (1990)
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RESULT 9
HUMLDLRA2/c
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ORIGIN
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AUTHORS
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                                                                                                   TGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGC
   HUMLDLRA2
                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987). Individual FH 295 carries two mutant LDL receptor alleles. The allele below was inherited from the far and includes a duplication of exons 2 through 8 that was presumably created by unequal chromosomal crossover involving Alu repeats in introns 1 and 8. The exact site of recombination cannot be determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 90)
Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alu-
recombination in a subject with familial hypercholesterolemia
Cell 48 (5), 827-835 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M15365.1 GI:187107
Alu repeat; LDL receptor; cell surface
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human (FH 295) fibroblast DNA, clone p295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             because the sequences of the Alu repeats in introns 1 and 8 of normal alleles are identical over a span of 26 nucleotides at the
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombination site
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                                                                                                                                                                                                                                             /note-"LDLR duplicated intron 1 (no splice 68); putative; does not fit consensus" 33 c 19 g 20 t cream of NheI site; chromosome 19p13.2-p13.1
 97
density
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p13.3"
                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                              /note="LDLR intron 8; G00-119-362"
                                                                                                                                                                                                                                                                                                                                                                               /gene="LDLR"
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100.0%; Pr
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lipoprotein receptor
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Pred. No.
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2.6e-07;
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2.6e-07;
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gene
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 07-JAN-1995
(LDLR), intron 5
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JOURNAL MEDLINE COMMENT

FEATURES

REFERENCE AUTHORS TITLE

SOURCE ORGANISM

SEGMENT

ACCESSION VERSION KEYWORDS

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RESULT 10
HUMLDLRDJ/c
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38; Conserv
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Chromosome 19p13.2-p13.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                      M14179.1 GI:187101
low density lipoprotein receptor-1; very low density lipoprotein.
Human fibroblast DNA, from patient FH-626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 261 (28), 13114-13120 (1986) 87008518
                                                                                                                        Analysis of the LDL-receptor gene of a patient with familial hypercholesterolemia (FH) revealed the deletion of exon 5 resulting from a homologous recombination between repetitive Alu sequences of
                                                                                                                                                                                                                       Hobbs,H.H., Brown,M.S., Goldstein,J.L. and Russell,D.W. Deletion of exon encoding cysteine-rich repeat of low density lipoprotein receptor alters its binding specificity in a subject with familial hypercholesterolemia J. Biol. Chem. 261, 13114-13120 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis of the LDL-receptor gene of a patient with familial hypercholesterolemia (FH) revealed the deletion of exon 5 resulting from a homologous recombination between repetitive Alu sequences of intron 4 and intron 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97)
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2 of 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRDJ 97 bp DNA PRI 27-APR-1993
familial hypercholesterolemia 626-a gene with a deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="deletion target sequence"
34 c 25 g 19 t
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/db_xref="taxon:9606"
/map="19pl3.3"
/oin(M14178.1:1..97,1..97)
/gene="LDLR"
        /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%; Pr/
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AUTHORS
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S79561/c
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S79560/c
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Db 79 TGCCTGTAATCCCAGCACTTTGGGAGGCCAAGCCAGG 43
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es 37; Conserv
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Chromosome 19p13.2-p13.1.
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101)
Bernard, O.A., Romana, S.P., Schichman, S.A., Mauchauffe, M.,
                                                                                                                                                                                                                                                                                           S79561 101 bp DNA PRI 27-JRAN-1996 GHRX [partial genomic duplication startpoint] (human, acute myeloid leukemia with trisomy 11 syndrome patient J, Genomic Mutant, 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 170933] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
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Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 101)
Bernard, O.A., Romana, S.P., Schichman, S.A., Mauchauffe, M.,
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HRX {intron 6} [human,
$79560
          Jonveaux,P. and Berger,R.
Partial duplication of HRX in acute leukemia with trisomy ll
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                             $79561.1 GI:1168042
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Partial duplication of HRX in acute leukemia with Leukemia 9 (9), 1487-1490 (1995)
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                                                                                                                                                                         human acute myeloid leukemia with trisomy 11 syndrome patient J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.1%; Score 37; DB 10; Length 101;
Similarity 100.0%; Pred. No. 8e-07;
37; Conservative 0; Mismatches 0; Indels
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/gene="HRX"
a 21 c
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34 c 23 g 18 t
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/db_xref="taxon:9606"
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BASE COUNT ORIGIN

Matches

COMMENT

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FEATURES

REFERENCE

AUTHORS TITLE

SOURCE ORGANISM

DEFINITION

<u>.</u>.

ACCESSION KEYWORDS

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ACCESSION
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HUMD6B03M3
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                                                                                         gene signature
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                                                                                                               Human HepG2 3'
D17279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 170936] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                Homo sapiens
                                                                                                                                        HUMD6B03M3
                                                                                                                                                                                                                                                                                                                                                                                          US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 40)
Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and Perkins, E. TRANSFORMATION ASSOCIATED RECOMBINATION CLONING Patent: WO 9801573-A 15-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
               Matoba, R
                                                                             Homo
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Similarity 100.0%; Pred. No.
36; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified
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95387660
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                                                                        sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
  Submission
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/db_xref="taxon:32644"
12 c 13 g
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/db_xref="taxon:9606"
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MboI cDNA, clone
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8e-07;
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28372 ACCICCGCCTCCCGGGTTCAAGCGATTCTCCTGCCT 28407
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                         l Similarity
36; Conserv
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Japan, 619-
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Query Match 0.1%; Score 36; Best Local Similarity 100.0%; Pred. No. Matches 36; Conservative 0; Mismatc
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1 (Dases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences

J. Mol. Biol. (1992) in press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human carcinoma
M87896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 51)
Matoba,R., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.
Matoba,R., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.
The addition of 5'-coding information to a 3'-directed cDNA library improves analysis of gene expression
Gene 146 (2), 199-207 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo Matoba, Osaka University. Institute for Molecular and Cellular Bio: 1-3, Yamada-oka, Suita, Osaka 565, Japan (E-mail:matoba@inherit.imcb.osaka-u.ac.jp, Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M87896.1 GI:174874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens male embryo carcinoma cDNA to other RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phone: 07747-5-2308
Fax: 07747-5-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology
Rizugawadai Kizu-cyo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-Jul-1993) to DDBJ by:
    Conservative
                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/clone_lib="Kiseru"
                                                                                                                                 /tissue_type="carcinoma"
27 c 33 g 1
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100.0%; Pred. No. 2.1
tive 0; Mismatches
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3. 2.5e-06;
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                     DB 9; Le
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clone CE221.
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Search completed: March 31, 2000, 06:36:34 Job time: 184343 sec

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Page 6

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed. s derived by analysis of the total score distribution.
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Intronic human MSH
Primer, RI-Not-T30
Primer MBTC from W
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Porcine reproducti
Splint oligonucleo
pV3TA-LTR oligonuc
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Oligonucleotide 43
Oligonucleotide 43
                             PCR suppression pr
Primer of the spec
EP-892047 Seq ID 1
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3' portion of cDNA
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cDNA synthesis pri
Primer Alu B corre
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Alu PCR primer 1.
Inter-Alu specific
     cDNA synthesis
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V19045/c
ID V19045;
AC V19045;
DT 28-JUL-1998 (first entry)
DE Alu PCR primer 2.
KW PCR; primer; amplification;
KW circular yeast artificial (
OS Synthetic.
OS Saccharomyces sp.
PN W09801573-Al.
PD 15-JAN-1998.
PF 09-JUL-1996; WO-U11478.
PR 09-JUL-1996; WO-U11478.
PR (USSH) US DET HEALTH & HI
PI Kouprina MV, Larionov VL, I
DR WF; 98-110234/10.
PT recombination using vector
PT yeast telomere and nucleic
PS Example 1; Page 45; 117pp;
CC This is the nucleotide sequence of DNA is known.
CC the creation and use of ci.
Ct to selectively clone specific sequence of DNA is known.
CC sequence of DNA is known.
        PR SON REPRESENTATION OF P SON REPRESENTATION OF PR SON REPRESENTATION OF P SON REPRESENTATION OF PROPERTY O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, present telomere and nucleic acid for recombination Example 1; Page 45; 117pp; English.

Consider the nucleotide sequence for the PCR primer used in the confidence of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the csequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

So Sequence 40 BP; 9 A; 8 C; 19 G; 4 T;
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Matches 40; Conservative
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4444
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Alu PCR primer 1.

PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.

Synthetic.

Saccharomyces sp.

MO9801573-A1.

MO9801573-A1.

15-JAN-1998.

09-JUL-1996; WO-U11478.
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09-JUL-1996; WO-U11478.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
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PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
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V19044;
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T93764
T98502
T88002
T88002
V24462
V24019
V35496
X19061
V83890
T17031
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Pred. No.
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Primer/probe used
cDNA synthesis pri
Primer used in iso
PCR primer for cho
PCR primer for Hum
Mouse calpain nCL-
Human PPAR-gamma o
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Human mitochondria
Knot probe P302 us
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Minimum Maximum

DB DB

seq

length:

8 105

Post-processing: Listing first 45

summaries

N_Geneseq_36:*

Total number of hits satisfying

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SUMMARIES

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V48090 V48091 T98523 Q93960 T39266

V15487 V15458

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Title: Perfect score:

US-08-852-495C-1_COPY_140000_170000 30001

Run

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OM nucleic

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nucleic search, using sw

model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Scoring Sequence:

table:

OLIGO_NUC

60.0,

311585 seqs, Gapop

125096042 residues Gapext 60.0

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RESULT 4
Q77890/c
ID Q77890 standard; cDNA; 30 BP.
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Best Local (
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Best Local
                                                                                                                                                                                                              24027 TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC 24061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telemere and nucleic acid for recombination

Example 1, Page 45, 17/pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                        claim 6; Page 6; 31pp; English.

Primer PDJ3 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can be used to detect genetic variation.

See 027389-027404 and 033141-033144.

Sequence 35 BP; 8 A; 10 C; 11 G; 6 T;
Neural thread protein AD10-7 cDNA 5' antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 92-284683/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase chain
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                             06-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-7AN-1993 (first entry)
Inter-Alu specific primer PDJ33.
Polymerase chain reaction; PCR;
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227391 standard; DNA; 35
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Kouprina NY, Larionov VL, Perkins EL, Resnick MA;
                                                                                                                                                                                      35 TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC 1
                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                           Similarity
35; Conser
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                                                                                                                                                                                                                                                                         0.1%; So larity 100.0%; I Conservative 0;
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vijg J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                   Score 35; DB 1;
Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repetitive element;
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                                                                                                                                                                                                                                                                           0;
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                                               Query Match
Best Local S
Matches 29
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20-APR-1994; U04321.
20-APR-1993; US-050559.
20-APR-1993; US-050559.
(GEHO) GEN HOSPITAL CORP.
De LA MONTE SM, Wands JR;
MPI; 94-341497/42.
     28388 TTCAAGCGATTCTCCTGCCTCAGCCTCCC 28416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                       Similarity
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                                                  Conservative
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                                                                       100.0%;
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                                                                    Score 29;
Pred. No.
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DB 1; 27;

Length 30; Indels

0; Gaps

<u></u>

Matches

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RESULT

T27744/C

ID 727744/S

AC 727744/S

AC 727744/S

DT 14.NOV-1996 (first entry)
DE Neural thread protein antisens
KW Alzheimer's disease; neuroecte
KW Alzheimer's disease; neuroecte
KW Alzheimer's disease; neuroecte
KW Monoclonal antibody; binding 1

OS Synthetic.
PN W09615272-Al.
PF 14-NOV-1995; U17111.
PF 14-NOV-1995; U17111.
PF 14-NOV-1994; U5-340426.
PR (OBHO) GEN HOSPITAL CORP.
PR 14-NOV-1994; W5-340426.
PR (OBHO) GEN HOSPITAL CORP.
PI Detection of neural thread properties of the properties of containing the properties of containing the properties of containing the properties of binding to the properties of containing the properties of containing the properties of containing the properties of all the capable of binding to the properties of antime containing the properties of a subject comprises (a) contact; CC is subject comprises (a) contact; CC is subject of binding to the properties of a subject of binding to the properties of binding the properties of a subject of binding to the properties of b
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PS Disclosure; Page 48; 238p; English.
CC A method for detecting the presence of neural thread protein (NTP)
CC A method for detecting the presence of neural thread protein (NTP)
CC subject comprises (a) contacting a sample from a human subject that
CC subject comprises (b) contacting a sample from a human subject that
CC capable of containing the NTP with at least one molecule
CC capable of binding to the protein; and (b) detecting any of the
CC molecule bound to the protein. The binding molecule is selected
CC from an antibody free of natural impurities, a monoclonal antibody
CC or a binding fragment of either of these. The method may be used for
CC diagnosing the presence of Alzheimer's disease, neuroectodermal
CC tumours and a malignant astrocytoma in a human. Expression of NTP
CC (See T2739-44)
CC (See T2739-44)
Sequence 30 BP; 8 A; 4 C; 14 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28388 TICAAGCGATICICCTGCCTCAGCCTCCC 28416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of neural thread proteins - to detect sporadic and familial Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and glioblastomas (Eng).
Disclosure; Page 48; 158pp; English.
077888-077890 are ADIO-7 neural thread protein (NTP) antisense oligonucleotides, that can be used to down regulate or inhibit the expression of the NTP gene. These oligonucleotides could be used in the treatment of the folowing conditions Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and glioblastomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-1996 (first entry)
Neural thread protein; NTP; diagnosis; detection;
Neural thread protein; NTP; diagnosis; detection;
Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;
monoclonal antibody; binding fragment; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of neural thread protein in diagnosis of disease - also NTP DNA and protein sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours; malignant astrocytomas; glioblastomas; 5' antisense therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 TTCAAGCGATTCTCCTGCCTCAGCCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzheimer's
in gene and
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TTCAAGCGATTCTCCTGCCTCAGCCTCCC

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TRESULT
T98500/c
ID T9850
AC T985
AC CDNA
KW Temp
KW PCR
KW PCR
Synth
FP 10-3-3-2
PR 03-3-2
PR 03-3-2
PR 03-3-2
PR 03-3-2
PR WPI:
PR W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PT primer to RNA, synthesising DNA and contacting with novel template PT primer to RNA, synthesising DNA and contacting with novel template PT claim 9; Page 29; 39pp; English.

CC T98497-T98520 represent primers used in the method of the invention. The CC method of the invention is for preparing DNA complementary to the 5'-end CC finer to the RNA molecule and synthesissing a first DNA strand CC complementary to at least a portion of the RNA molecule, and contacting the RNA molecule with a template switching oligonucleotides (TSO) (such as T98426) having a pre-selected nucleotide sequence at its 5'-end and at least 1 riboguanine residue at its 3'-end, where the TSO binds the 5'-end cf the RNA molecule and serves as a template for the extension of the CC 3'-end of the first DNA strand. The method can be used for the synthesis and cloning of full length cDNA, or fragments, that correspond to the CC construct cDNA libraries from nanogram quantities of total or poly A+ CC RNA. The TSO allows for negative selection against cDNA that are not complementary to the 5'-end of the template RNA, while allowing full CC length cDNA to be readily selected.

Sequence 55 BP; 10 A; 5 C; 7 G; 33 T;
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Best Local s
Matches 29
                                                                                  Synthetic.
W09724455-A2.
10-JUL-1997.
10-JAN-1997: U00368.
03-JAN-1996: US-582562.
(CLON-) CLONTECH LAB INC.
Chenchik A, Diatchenko L,
WPI: 97-363690/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26680 АААААААААААААААААААААААААА
                                                                                                                                                                                                                                                                                                                    Template switching oligonucleotide; RNA/DNA hybrid; DNA preparation, cDNA synthesis primer; cDNA cloning; cDNA library construction; pcR primer; amplify; ss.
Preparation of cDNA from RNA molecules primer to RNA, synthesising DNA and conswitching oligo:nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1998 (first entry) cDNA synthesis primer Fr-T30NN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CLON-) CLONTECH LAB INC.
Chenchik A, Diatchenko I
WPI; 97-363690/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T98500;
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03-JAN-1997; U00368.
03-JAN-1996; US-582562.
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Template switching oligonucleotide; RNA/DNA hybrid; DNA preparation, CDNA synthesis primer; cDNA cloning; cDNA library construction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preparation of cDNA from RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98500 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 0.1%; s
l Similarity 100.0%;
29; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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                                                                                                             Siebert P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB; Pred. No. 23; 0; Mismatches
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DNA and conta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                           les - by annealing cDNA synthesis contacting with novel template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              les - by annealing cDN
contacting with novel
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23;
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28

CCTGGGCGACAGAGCGAGACTCTGTCTC

RESULT

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19152 CCTGGGCGACAGAGCGAGACTCTGTCTC

Query Match
Best Local Similarity
Matches 28; Conser

Conservative

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Mismatches 19179

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Indels

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Score Pred.

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Length

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RESULT .
T12509/c
TD T12509 standard; F
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CC T98497-T98520 represent primers used in the method of the invention. The CC method of the invention is for preparing DNA complementary to the 5'-end CC of an RNA molecule. The method comprises annealing a cDNA synthesis CC complementary to at least a portion of the RNA molecule, and contacting CC complementary to at least a portion of the RNA molecule, and contacting CC as T98426) having a pre-selected nucleotide sequence at its 5'-end and at CC least 1 riboguanine residue at its 3'-end, where the TSO binds the 5'-end CC is the RNA molecule and serves as a template for the extension of the CC 3'-end of the first DNA strand. The method can be used for the synthesis CC complete sequence of the 5'-end of the many molecule. It can be used to the CC construct cDNA libraries from nanogram quantities of total or poly A+ CC RNA. The TSO allows for negative selection against cDNA that are not CC complementary to the 5'-end of the template RNA, while allowing full CC length cDNA to be readily selected.

Sequence 58 BP; 8 A; 5 C; 9 G; 34 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #888888888888888888
PT Quantifying genomic DNA by amplification of repetitive sequences -
prin presence of internal standard, then comparing amts of amplified
prince DNA and standard, partic. for quality control of recombinant
prince DNA and standard, partic.
prince DNA in a sample set.

Claim 13; Page 14; 41pp; German.

Primers T12508-9 are used to amplify a 146 bp fragment of an Alu repeat
csequence in a novel method of quantitating genomic DNA in a sample. The
novel method features the addition of a known amount of an internal
standard nucleic acid which is different from the test nucleic acid in
cat least one detectable feature. The template for these primers is the
plasmid pAlu-wt which comprises plasmid pCRII contg. nucleotides 148-294
of the Alu repeat sequence given in Nucleic Acid Res., 18 (1990) 6793.
The method is esp. useful for the detection of contaminating DNA in the
manufacture of therapeutic prods.
Sequence 28 BP; 5 A; 9 C; 9 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                         Kohl J
                                                                                                                                                                                                                                                                                       WPI; 96-069063/08.
                                                                                                                                                                                                                                                                                                                                                                26-SEP-1994; 001830.
26-SEP-1994; AT-001830.
                                                                                                                                                                                                                                                                                                                                                                                                                                              quantitation; synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer Alu B
Primer; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                        AT9401830-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1996
                                                                                                                                                                                                                                                                                                                                              (IMMO ) IMMUNO AG.
                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity 100 29; Conservative
                                                                                                                                                                                                                                                                                                                          Falkner F, Haemmerle T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
corresp. to bases 294-267.
polymerase chain reaction; an
; internal standard; plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB
Pred. No. 22;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                          Himmelspach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           amplification; Alu repeat; ss;
d; contamination; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                       is the 148-294 6793.
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RESULT 10
Q73570/c
ID Q73570 standard; DNA; 32 BP.
AC Q73570,
PT 25-UTW-1995 (first entry)
DE Enhancer element er-3 conserved basepair sequence.
KW Enhancer element; carcinoma; tumor; cancer; SLPI gen
KW secretory leukoprotease-inhibitor gene; cytokeratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALD DECEMBER OF THE PROPERTY O
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Best Local
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24-MAR-1994; U03197.
24-MAR-1993; US-035435.
(UABR-) UAB RES FOUND.
Garver RI, Sorscher EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9421118-A.
29-SEP-1994.
24-MAR-1994; U03197.
24-MAR-1993; US-0354
                                                Garver RI, Sorscher EJ;

WPI; 94-316537/39.

DNA construct for treating human carcinoma - includes a cancer-therapeutic gene under the control of a promoter and a gp. of enhancer sequences

Claim 1; Fig. 6; 54pp; English.

This enhancer element is part of a DNA construct used for treating human carcinoma which contains a cancer therapeutic protein under the control of a promoter and 3 enhancer sequences in a specific 5'-3' order. This enhancer element is derived from the flanking region of the human epithelial cell cytokeratin-8 gene.

Sequence 32 BP; 7 A; 1 C; 8 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of enhancer sequences
Claim 1; Fig.6; 549p; English.
This enhancer element is part of a DNA construct used for treating
thuman carcinoma which contains a cancer therapeutic protein under
the control of a promoter and 3 enhancer sequences in a specific 5'-3'
order. This enhancer element is derived from the flanking region of
the human epithelial cell cytokeratin-8 gene.
Sequence 32 BP; 7 A; 1 C; 8 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 94-316537/39.

DNA construct for treating human carcinoma - includes a cancer-therapeutic gene under the control of a promoter and a gp. of enhancer sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UABR-) UAB RES FOUND
Garver RI, Sorscher I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhancer element er-3 conserved basepair sequence. Enhancer element; carcinoma; tumor; cancer; SLPI g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q73570;
25-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q73570 standard; DNA; 32 BP.
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Similarity 100.0%;
28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 29
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/label=
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/label= pyrimidine
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pyrimidine
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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205168/c
ID 025168/c
ID 025168/c
AC 0251
DT 2510
DE Sequ
KW Hums
ON Synth
PN 000/o
PN 000/o
PP 23--
PP 23--
PP 621-
PP 621-
PP 621-
PP 6411
DR WP1
PP 6411
DR WP1
PP 6411
PP 
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T04081/c
os Synthétic.

No. 197242700-A.

PN 197242700-A.

PD 19-5EP-1995.

PF 04-MAR-1994; 059906.

PR 04-MAR-1994; JP-059906.

PR 04-MAR-194; JP-05906.

PR 04-MAR-194; JP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 28
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AA (CORN) UNIV NEW YORK MT SINAI.

AS SCHOOL MEDICINE.

AN SCHOOL MEDICINE.

I Gelman IH, Laurence JC;

RWPI; 94-026200/03.

Example; page 7; 75pp; English.

Comparison of First strand was example; page 7; 75pp; English.

Comparison of First Strand was amplified by PCR using converted into dsDNA and this cDNA was amplified by PCR using converted into dsDNA and this cDNA was amplified by PCR using converted the dsDNA and this cDNA was amplified by PCR using converted the dsDNA and this cDNA was amplified by PCR using converted the dsDNA was amplified by 
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Best Local
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23-JUN-1993;
24-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4696 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-1996 (first entry)
Trypsin inhibitory protein cDNA antisense primer-1.
Trypsin inhibitor; human T98G cells; pancreatitis; shock; DIC;
Trypsin; inhibitor; human T98G cells; pancreatitis; shock; DIC;
Trypsin; inhibitor; human T98G cells; pancreatitis; shock; DIC;
Trypsin; inhibitor; shock in the state of the st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1994 (first entry)
Sequence of primer for PCR amplification of HIV-LP Pt.1 isolate
Human immunodeficiency virus; HIV-LP; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q55168 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04081 standard; DNA; 48 BP
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US-903421
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tive 0;
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Pred. No.
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RESULT
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AC TE
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                                                                                                                                                                                                                                                                      PT regulating, immunomodulating and many other activities are Disclosure; Page 86; 139pp; English.

CC The present sequence encodes a portion of E. novel human secreted protein CC deposited under accession number ATCC 98026. The secreted protein can be used to determine biological activity, to raise antibodies, as tissue that modulate their interactions and as nutritional supplements. It may called the provided in the specification. Typical of these are induction of other cytokines; immunostimulating/immunosuppressant cartivities (e.g. for treating human immunodeficiency virus infection, carter, autoimmune diseases and allergy); regulation of haematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation of prowth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumours); haemostiatic or thrombolytic (e.g. for treating infections, tumours); haemostiatic or thrombolytic activity (e.g. for treating infections; tumours); haemostiatic or thrombolytic canti-inflammatory activity (e.g. for treating septic shock, Crohn's cartivity (e.g. for treating septic shock, Crohn's cativity (e.g. for treating septic shock, Crohn's cartivity (e.g. for treating sportasis or other hyperproliferative disease; for regulation of metabolism, behaviour, and cardid in gene therapy procedures.

Sequence 49 BP; 40 A; 2 C; 6 G; 1 T;
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Matches 28
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                                                                                                                                  Query Match
Best Local Similarity
Matches 28; Conserv
T88080;
14-MAY-1998 (first entry)
3' portion of cDNA clone encoding secreted
                                                   T88080 standard; cDNA; 49 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New secreted proteins encoded clones present in ATCC 98026 - possibly having cytokine, cell proliferation/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spaulding V;
WPI; 97-526460/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC.
Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1997; U06139.
18-APR-1996; US-634325.
(GEMY) GENETICS INST I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein AK533 3' portion including the polyA tail Human; secreted protein; ATCC 98026; cytokine; immunomodulation; cell proliferation; differentiation; regulation; ds.
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Best Local S
Matches 28
                                                                     WO9837241-A1.
27-AUG-1998.
23-FEB-1998; U03725.
18-JUN-1997; US-050109.
24-FEB-1997; US-038798.
(TMTE-) TM TECHNOLOGIES I
Benight AS, Faldasz BD, L
WPI; 98-467588/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting telomerase activity - without the need for polymerase chain reaction amplification, can be adapted to assay for telomy inhibitors
                                                                                                                                                                                                                                                                                                                                             18-NOV-1998 (first entry)
DNA detector sequence used in a telomeric activity assay.
Telomerase; telomeric repeat sequence; carcinogen; seneso
                                                                                                                                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                         V54636;
V54636;
                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human and murine secreted proteins - useful to research or treat diseases or disorders related to their function Disclosure; Page 86; 140pp; English. The present sequence is the 3' portion of a cDNA clone encoding a human secreted protein, which may have nutritional uses, or cytokine and cell proliferation/differentiation, immune stimulating or suppressing, haematopoiesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and the contraction of the cont
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WPI; 97-526459/48.
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11-APR-1997; U06042.
12-APR-1996; US-631184
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3' portion; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 53 BP
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/note= "Forms a double-stranded region
bases 38-60 of V54639"
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                                                                                                                                                                                                                                                                                                                                                          senescence;
                          for telomerase
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9pp;

English

Page 6

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                                                                                                                                                  Search completed: March 31, 2000, 10:14:26 Job time: 195864 sec
                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a method for detecting the presence of telomerase cc activity. The method comprises of (a) providing a test nucleic acid, ce 9. the nucleic acid sequence shown in V54635, that will be elongated by telomerase; (b) incubating the test nucleic acid with the sample containing a telomerase; and (c) detecting the elongated concleic acid, e.g. see V54639, using a detector sequence such as the cc present one or the sequence shown in V54637. The test nucleic acid, ci immobilised on a solid support, comprises of a hairpin and/or a telomeric repeat sequence, prior to elongation by telomerase. Detection cc of telomeric repeat sequence, prior to elongation by telomerase. Cc carcinogenicity and senescence in cells. The assay is also claimed to be useful for determining the effects of compounds on telomerase activity is claimed to be useful for determining the effects of compounds on telomerase activity. The identified telomerase inhibitors might then be useful in cc activity. The identified telomerase inhibitors might then be useful in cc sequence 53 BP; 7 A; 12 C; 1 G; 33 T;
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   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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PCT-US95-17111A-69

US-08-450-673C-6

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US-08-450-673C-6

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Sequence 2, Appli	Sequence 2, Appli	Patent No. 5478746	•	•	Sequence 70, Appl	Sequence 70, Appl	Sequence 70, Appl	•	•	•	-	-	•	•	•	•	•	•
	0.1 42 1 US-08-287-164-2 Sequence 2,	0.1 42 1 US-07-875-167-2 Sequence 2, 0.1 42 1 US-08-287-164-2 Sequence 2,	0.1 33 7 5478746-1 Patent No. 547 0.1 42 1 US-07-875-167-2 Sequence 2, P 0.1 42 1 US-08-287-164-2 Sequence 2, P	42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 43 27 0.1 33 7 5478746-1 Patent No. 547 44 27 0.1 42 1 US-07-875-167-2 Sequence 2, 4 45 27 0.1 42 1 US-08-287-164-2 Sequence 2, 4	41 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 43 27 0.1 33 7 5478746-1 44 27 0.1 42 1 US-07-875-167-2 Sequence 2, 1 45 27 0.1 42 1 US-08-287-164-2 Sequence 2, 1	40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, 41 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 43 27 0.1 33 7 5478746-1 44 27 0.1 33 7 5478746-1 547 0.1 42 1 US-07-875-167-2 Sequence 2, 1 548 27 0.1 42 1 US-08-287-164-2 Sequence 2, 1	39 28 0.1 78 4 US-08-450-673C-70 Sequence 70, 40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, 41 28 0.1 78 6 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PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 43 27 0.1 33 7 5478746-1 Sequence 70, 44 27 0.1 42 1 US-08-287-164-2 Sequence 2, 44 28 0.1 78 6 PCT-US95-17111A-70 Sequence 2, 44 27 0.1 42 1 US-08-287-164-2 Sequence 2, 44 28 0.1 78 6 PCT-US95-17111A-70 Sequence 2, 44 27 0.1 42 1 US-08-287-164-2 Sequence 2, 44 28 0.1 78 6 PCT-US95-17111A-70 Sequence 2, 44 28 0.1 78 6 PCT-US95-17111A-70 Sequence 2, 44 28 0.1 78 6 PCT-US95-17111A-70 Sequence 2, 44 28 0.1 95 0.	34 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 35 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 36 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 37 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 39 28 0.1 78 4 US-08-450-673C-70 Sequence 70, 40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, 41 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 43 27 0.1 33 7547876-1 Sequence 2, 44 27 0.1 42 1 US-07-875-167-2 Sequence 2, 45 27 0.1 42 1 US-08-287-164-2 Sequence 2, 47 25 28 28 28 28 28 28 28 28 28 28 28 28 28	33 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 34 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 35 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 36 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 37 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 39 28 0.1 78 4 US-08-340-26D-70 Sequence 70, 40 28 0.1 78 4 US-08-450-573C-70 Sequence 70, 41 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 43 27 0.1 33 7547876-1 Sequence 2, 14 44 27 0.1 42 1 US-08-287-164-2 Sequence 2, 14	32 28 0.1 60 4 US-08-450-673C-58 Sequence 58, 33 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 34 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 35 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 36 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 37 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 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PCT-USS5-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-USS5-17111A-70 Sequence 70, 43 27 0.1 42 1 US-08-287-164-2 Sequence 2, 145 27 0.1 42 1 US-08-287-164-2 Sequence 2, 145 27 0.1 42 1 US-08-287-164-2	30 28 0.1 60 4 US-08-340-426D-58 Sequence 58, 31 28 0.1 60 4 US-08-450-673C-58 Sequence 58, 32 28 0.1 60 4 US-08-450-673C-58 Sequence 58, 33 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 34 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 35 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 36 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 37 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 39 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 39 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 41 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 27 0.1 42 1 US-08-287-164-2 Sequence 2, 14 25 0.1 42 1 US-08-287-164-2 Sequence 2, 14 25 0.1 42 1 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Sequence 58, 30 28 0.1 60 4 US-08-340-426D-58 Sequence 58, 31 28 0.1 60 4 US-08-450-673C-58 Sequence 58, 31 28 0.1 60 6 US-08-450-673C-58 Sequence 58, 32 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, 33 28 0.1 78 3 US-08-45-57C-70 Sequence 58, 33 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 36 28 0.1 78 3 US-08-454-557C-70 Sequence 70, 36 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 37 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 38 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 39 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 39 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 39 28 0.1 78 4 US-08-340-426D-70 Sequence 70, 41 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, 42 27 0.1 42 1 US-08-287-164-2 Sequence 2, 2, 2, 45 20 0.1 42 1 US-08-287-164-2 Sequence 2, 2, 2, 3, 45 20 0.1 42 1 US-08-287-164-2

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US-08-454-557C-57
                                                          Query Match
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

ZIP: 2005-3924

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIg, Steven R.
REFERENCE/DOCKET NUMBER: 06.09.3840003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                9496 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCACC 9533
                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                          LENGTH:
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E: Sterne, Kessler, Goldstein & 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                            60 base pairs
                                                                   Conservative
                                                                                                                                                                         both
                                                             0.1%; Scc.
/ 100.0%; Pr
                                                                   Score 38; DB
s; Pred. No. 0.0
0; Mismatches
                                                                                 0.0042;
                                                                                                      DB 3;
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RESULT 2
US-08-340-426D-57
US-08-340-426D-57
Sequence 57, Application US/08340426
Patent No. 5948634
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-340-426D-57
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US-08-450-673C-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.1%; Score 38; DB 4; Length 60; Best Local Similarity 100.0%; Pred. No. 0.0042; Matches 38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Patent No. 5948888
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/08450673C Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING REJEASE #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/340,426D FILING DATE: 14-NOV-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE,DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                     TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                       STREET: LLVC
CITY: Washington
                                                                                  COUNTRY:
                                                                                                                                                                    ADDRESSEE:
                                                              20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08340426D
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1100 New York Avenue, Suite 600
                                                                                                                                           sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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US-08-450-673C-57
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 08/340,426
APPLICATION NUMBER: 08/340,426
APPLICATION NUMBER: 14 NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R, 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNALIANDE AND ANAME: LUdwig, Steven N. AMAE: Ludwig, Steven N. AMAE: 16.203
REGISTRATION NUMBER: 36.203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 171-2540
                                                                                                              TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
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LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
COMPUTER: IEM FC COMPATION
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: de la Monte,
APPLICANT: Wands, Jack R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCACC 48
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COUNTRY: U.S.A.
ZIP: 20005-3934
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                                                       STRANDEDNESS:
                                                                                                ENGTH:
                                                         nucleic acid EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de la Monte, Suzanne
                                         both
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100.0%; Pred. No. 0.004;
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US-08-454-557C-69; Sequence 69, App.; Patent No. 5830
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                                                                                                                          RESULT 6
US-08-340-426D-69
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                                                                                                                                                                                                                                                 Query Match
Best Local s
Matches 38
                                                                         Sequence 69, Application US/08340426D Patent No. 5948634 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                     9496 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCACC 9533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9496 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACC 9533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                             APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                       GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                 1 Similarity 100.
38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                         76 base pairs
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                                                                                                                                                                                                                                             0.1%; Dur
100.0%; Pr
'''' 0;
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100.0%; Pred. No.
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b; Pred. No. 0.0
0; Mismatches
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0.0042;
                                                                                                                                                                                                                                                                 DB 3;
0.004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 69, Application US/08450673C Patent No. 5948888
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA: US/08/450,673C
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT_INFERMATION:
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9496 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCACC 9533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                        STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                        Washington
                                                       Ludwig, Steven R.
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                                                                                                                                                                                                                                                                                                                                          2: Sterne, Kessler, G
1100 New York Avenue,
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                              Kessler, Goldstein & Fox P.L.L.C.
ork Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                       121
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                       0609.3840004
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                                                                                                                                                                        Version
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TOPOLOGY:
US-08-450-673C-69
                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
REFERENCE/DOCKET NUMBER: 0609.3840002
RELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.1%; Score 38; DB 4; Best Local Similarity 100.0%; Pred. No. 0.004; Matches 38; Conservative 0; Mismatches
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SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 69 Application PC/TUS9517111A

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.

APPLICANT: Wands, Jack R.

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Detection of Alzheimer's Disease

TITLE OF INVENTION: Detection of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessier, Goldstein & Fox P.L.L.C.
ADDRESSEE: Sterne, Kessier, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                             ;
PCT-US95-17111A-69
RESULT 9
US-08-454-557C-6/c
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: PATENTION DATA:
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/3/2 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                   STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATABLE COMPUTER: IBM PC COMPATABLE COMPUTER: IBM PC COMPATABLE PATENTING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: US/08/454,557C
APPLICATION NOWBER: US/08/454,557C
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-195
FILING DATE: 30-MAY-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08454557C Patent No. 5830670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: (102) 371-2540
INFORMATION FOR SEQ ID NO: (100) SEQUENCE CHARACTERISTICS: LENGTH: 30 base pair
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US-08-340-426D-6/C
US-08-340-426D-6/C
Sequence 6, Application US/08340426D
; Sequence 6, Seption US/08340426D
; Patent No. 5948634
; PATENTAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O.1%; Score 29; DB 3; Query Match 0.1%; Score 29; DB 3; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LIGWIG, Steven R.

NAME: TURNBER: 36.203
REGISTRATION UNMBER: 06
REFERENCE/DOCKET NUMBER: 06
REFERENCE/TON INFORMATION: TELECOMMUNICATION 176.2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                          NERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SECUENCES: 121
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                APPLICATION DATA:

TRENT APPLICATION DATA:

US/08/340,426D
                                                                                                                                                                         STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                                                                                           TY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid EDNESS: both
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Wands, Jack R.
                                                                                                                                                                                                                                          E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
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ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0609.3840003
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14-NOV-1994

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RESULT 11
US-08-450-673C-6/c
Sequence 6, Application  
Result No. 59488;
Patent No. 59488
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                                                                                                                                                                                                                      CLASSIFICATION: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
(202) 371-2600
Ouery Match 0.1%;
Best Local Similarity 100.0%;
Matches 29; Conservative
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                             TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 6:
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MEDITM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 TTCAAGCGATTCTCCTGCCTCAGCCTCCC 2
                                                                                                                    LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/450,673C FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1
CLASSIFICATION:
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20005-3934
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Ludwig, Steven R.
ATION NUMBER: 36,
                                                                                                          both
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00 New York Avenue,
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                Score 29;
Pred. No.
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                  DB 4;
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                                   Length 30;
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US-08-778-494B-67/c
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PCT-US95-17111A-6/c
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 29
                                                                                                                                                              Sequence 67, Application US/08778494B Patent No. 5962272 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
COUNTRY: U.S.A.
COUNTRY: 2005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PBM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                   28388 TTCAAGCGATTCTCCTGCCTCAGCCTCCC 28416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equence 6, Apprication:
                         APPLICANT: Siebert, Paul TITLE OF INVENTION: METHODS TITLE OF INVENTION: CLONING NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                   30 TICAAGCGATICTCCTGCCTCAGCCTCCC 2
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FILING DATE: 14-NOV-199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                           Chenchik, Alex
Zhu, York
Diachenko, Luda
2: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/340,426
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                                                                                  AND COMPOSITIONS FOR FULL-LENGTH CDNA
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                    Indels
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COUNTRY:

USA

Gainesville Florida

APPLICATION NUMBER: US/C

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TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 67:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPUTER: DOS
COMPUTER: TBM PC COMPUTER: 
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OPERATING SYSTEM: PC-DOS/MS-DOS
OSOTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTIAN DATA:
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: CL
REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/582,562
PILING DATE: 03-JAN-1996
PILING DATE: 03-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chencuary,
APPLICANT: Zhu, York
APPLICANT: Diachenko, Luda
APPLICANT: Stebert, Paul
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: FORM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/582,562
APPLICATION NUMBER: 03-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ААРАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАТА 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LE OF INVENTION: METHODS AND COMPOSITIONS FOR FULL-LENGTH CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.1%;
1 Similarity 100.0%;
29; Conservative
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2421 N.W. 41st Street, Suite A-1
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                                                                                                                            ....ER: US/08/778,494B
03-JAN-1997
N: 435
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; Pred. No. 2.1;

 Mismatches

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US-08-454-557C-91/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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US-08-454-557C-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
FILING DATE: 30-MAY-1995
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
CLASSIFICATION:
                                                                                                                                                   Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
REFERENCE/TOKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1100RMATION:
TELECOMMUNICATION 171-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                24038 TGTAATCCCAGCACTTTGGGAGGCTGAGG 24066
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REGISTRATION NUMBER:
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TOPOLOGY: 11; MOLECULE TYPE: US-08-778-494B-67

SEQUENCE CHARACTERISTICS: LENGTH: 55 bases

TYPE: nucleic acid
STRANDEDNESS: single

linear

Query Match Best Local

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US-08-778-494B-109/c

patent No. 5962272 GENERAL INFORMATION: Sequence 109, App Sequence 109, App Sequence 109, App

CORRESPONDENCE

ADDRESS

DDRESSEE:

STREET: 2421 N.W. CITY: Gainesville STATE: Florida

UNTRY:

USA

APPLICATION NUMBER:

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NUMBER OF SEQUENCES:

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Search completed: March 31, 2000, 10:04:17 Job time: 195319 sec

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 97)
Hillier,L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
         Unpublished (1995)
On May 9, 1995 this sequence
Contact: Wilson RK
                                    Wilson, R.
The WashU-Merck EST Project
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AA654896 nt61b07.s
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                                                                  Calfrech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75; Pasadena,
Tel: 626 796 7066
Fax: 626 395 4901
Email: ungdash tree caltech.edu
Clones are available from Research Genetic
                                                                                                                                                                  Eutheria; Primates; Catarrhini; Homin (bases 1 to 102)

Kim.U.-J., Adams,M.D. and Simon,M.I. Determination of clone end sequences
                                                                                                                                                                                                                                                        genomic survey sequence.
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Similarity 100.0%;
45; Conservative
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full_length read
                                                end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Contact: Ung-Jin Kim
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                                                                    (info@resgen.com). BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208

Fax: 301 838 0208
  L Similarity
43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org

Clones are derived from the human BAC library RFCI-11. For BAC

Clones are derived from the human BAC library RFCI-11. For BAC

Clones are derived from the human BAC library RFCI-11. For BAC

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onpublished (1997)
Other_GSSs: RPCII1-4N6.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 102)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P.
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
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B48088.1 GI:2600325
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                                                                                                            /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
a 24 c 25 g 21 t
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/db_xref="taxon:9606"
/clone="669F15"
                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="RPCI-11-4N6"
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7501469"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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100.0%; Pred. No.
0.1%; Score 43; DB 81;
100.0%; Pred. No. 0.0038;
tive 0; Mismatches 0
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sequence.
T52775
                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
On May 8, 1995 this sequence version replaced g1:801221
Contact: Robert Strausberg, Ph.D.
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oe02g07.s1 NCI_CGAP_Ov2
similar to contains Alu
AA873656
                                                   ya79d08.rl
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 61)
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                                    IMAGE: 67887
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pamp10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Ov2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1384764"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="ovary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                  Stratagene ovary (#937217) Homo sapiens cDNA clone 7 5' similar to contains Alu repetitive element, mR
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similar to contains Alu r
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AA715942.1 GI:2728716
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ьикатуота; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 95)
Hillion r
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 72)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTs: ya79d08.sl
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/db_xref="GDB:504144"
/db_xref="taxon:9606"
/clone="IMAGE:67887"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
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 Washington University School of Medicine
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AUTHORS
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Kucaba, T., Lacy, M., Le, M., Le, N., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Mardis, E., Moore, B., Morris, M., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T63772 105 bp mRNA EST 17-FEB-199: yc21f01.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81337 3' similar to contains Alu repetitive element; r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                               Generation and analysis of Genome Res. 6 (9), 807-828
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R.
Contact: Wilson RK
                                                                                                      and Marra, M.
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h quality sequence stop: 59.
    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: breast; Vector: pAMP10; mRNA made from normal breast ductal tissue, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

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/db_xref="taxon:9606"
/clone="IMAGE:1235843"
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40; Conserv
Insert Length: 451 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 50.
                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Unpublished 1997)
On Jan 17, 1998 this sequence version replaced gi:1900439
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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similar to
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                                                                                                                                                     cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 513
                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
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/clone="IMAGE:81337"
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/sex="male"
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Class: BAC ends.
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/note-"Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:1385090"
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                     'lab_host-"DH10B"
                                                                                                                                                                                   /tissue_type="ovary"
                                                                                                                                                                                                                                     clone_lib="NCI_CGAP_Ov2"
                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
29 g
  31 t
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734 GAGAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAG 772 Score 39; Pred. No. Mismatches DB 39; 0 Length 97; Indels 0

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Unpublished (1998)
Other_GSSs: CIT-HSP-2042J24.TF Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C. B80126 102 bp DNA CIT-HSP-2042J24.TR CIT-HSP Homo sapiens Use of a random BAC End Sequence Database for Sequence-Ready Map Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. GSS 24-OCT-1998 genomic clone 2042J24,

9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC Contact: Mark Adams
Department of Eukaryotic Genomics http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Institute for Genomic Research /organism="Homo sapiens"
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/note="Vector: pBeloBAC11; Location/Qualifiers /clone_lib="CIT-HSP" 19 g 3 MD 20850, USA Site_1:

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                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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C05051 Human heart cDNA
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104)
1 (bases 1 to 80)
Lanfranchi.G., Muraro,T., Caldara,F., Pacchioni,B., Pallav Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a
                                                                                                                                    F24490.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yusuke Nakamura
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                            /Clone="3NHC4544"
/Clone_lib="Human heart cDNA (YNakamura)"
/dev_stage="adult"
/note="Organ: heart; normalized direction:
from adult heart"
26 c 37 g 17 t
                                                                                                                                    GI:4810116
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/db_xref="taxon:9606"
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7P05B09 Chromosome 7 Pla
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On Jun 5, 1998 this sequence version Contact: Valle G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRIBI Biotechnology Centre
             Email: egreen@nhgri.nih.gov
Plate: 05 row: B column:
Seq primer: -21M13 (ABI).
                                                                                                                                 On Sep 12, 1996 this sequence version Contact: Eric D. Green
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                                                           Tel: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                               Homo sapiens
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/db_xref="taxon:9606"
/clone="s4000013A06"
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Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2.
                                                                                                                                         Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L., Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D. 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries Genome Res. 7 (3), 281-292 (1997)
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                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 96)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA252633 100 bp mRNA EST 12-MAR-1997 aq43g05.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632504 5' similar to contains Alu repetitive element;contains element MER22 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                      Putative full length read
The vector to vector length is 101
Seq primer: -28ml3 revl ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 5, 1995 this sequence version replaced Contact: Wilson RK
                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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/lab_host="E. coll strain DHS alpha"
/note="Organ: placenta; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."
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/db_xref="taxon:9606"
/clone="7P05B09"
                                                    /db_xref="taxon:9606"
/clone="IMAGE:632504"
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                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:5182587"
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  /clone_lib="Stratagene hNT neuron (#937233)"
/dev_stage="hNT neurons"
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Unpublished (1995)
On Apr 14, 1993 this sequence version
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1 (bases 1 to 101)

1 (bases 1 to 101)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., LeM., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rohlfing,T., Rohlfing,T.,
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zal2a02.rl Soares fetal
IMAGE:292298 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dr.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GRAFTCGGCGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:3800071"
/db_xref="taxon:9606"
/clone="IMAGE:292298"
                                                                                                                                                                                                                                                                                                                                                                      /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares fetal liver spleen lNFLS"
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hes 37; Conservative
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                                                          ch 0.1%; Score 36; DB 28; Length 74; I Similarity 100.0%; Pred. No. 0.64; 36; Conservative 0; Mismatches 0; Indels
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National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74)

Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L., Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.

2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries
Genome Res. 7 (3), 281-292 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: egreen@nhgri.nih.gov
Plate: 01 row: E column: 11
Seg primer: -21M13 (ABI).
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Contact: Eric D. Green
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/db_xref="taxon:9606"
/clone="7T01E11"
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Database :

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Scoring table: Sequence:

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Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and Ferkins, E. TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING PATENT: WO 9801573-A 15-JAN-1998;
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1 (bases 1 to 40)

1 (bases 1 to 40)

1 (bases 1 to 40)

Resnick,M.A., Larionov,V.L., Kouprina,N.TRANSFORMATION-ASSOCIATED RECOMBINATION PATENT: WO 9801573-A 15-JAN-1998;

US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A68621 40 bp DNA
Sequence 1 from Patent WO9801573.
A68621
A68621.1 GI:4759648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
36; Conserv
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D. Alu RNA transcripts in human embryonal carcinoma c post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                             Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 103)
                                                                                                                      M87896.1
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                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 40)
Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and Perkins, TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING Patent: WO 9801573-A 15-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unidentified
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unidentified
                                                                                               Homo sapiens male embryo carcinoma
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llarity 100.0%;
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12 c 13 g
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12 c 13 g
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                                                                                                                                                                                                                                                                                                                                                    synthetic construct.
synthetic construct
artificial sequence.
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                                                                                           synthetic construct
synthetic construct
artificial sequence.
                                                                                                                                     inter-Alu specific
A25212
                                                                                                                                                                                                                                                                                                                  METHOD OF DETECTING DNA SEQUENCE VARIATION Patent: WO 9213101-A 3 06-AUG-1992; Location/Qualifiers
                                                          METHOD OF DETECTING DNA SEQUENCE VARIATION Patent: WO 9213101-A 3 06-AUG-1992;
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Similarity 100.0%;
35; Conservative (
                                                                                   ificial sequence. (bases 1 to 35)
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/dev_stage="embryo"
/sex="male"
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/db_xref="taxon:32630"
10 c 11 g 6 t
                                                Location/Qualifiers
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27 c 33 g 1
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/db_xref="taxon:9606"
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                /db_xref="taxon:32630"
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Pred. No. 3.1e-06;
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DNA (pdj33) from patent WO9213101.
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patent WO9213101.
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19729 TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC 19763
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"DETECTING METHOD FOR DNA ARRANGEMENT VARIATION";
Patent number JP 1995115999-A/3, 09-MAY-1995.
INGENII BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified unclassified.
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Artificial sequences.
JP 1995115999-A/3
09-MAY-1995
22-MAY-1995
70-MAY-1995
70-MAY-1995
70-MAY-1995
70-MAY-1995
70-MAY-1992
                                                                                                                                                                                                                                                                                                                    ANDOREASU HERARUDOUSU AITSUTERURINDEN, YA C12Q1/68,C12N15/00,G01N27/447,G01N27/447; strandedness: Single;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified unclassified
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08-OCT-1997 (Rel. 52, Last upd
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Artificial sequences.
Jp 1995115999-A/3
09-MAY-1995
22-MAY-1992 JP 1992130668
22-MAY-1992 JP 1992130668
ANDOREASU HERARUDOUSU AITSUTERURINDEN, YA C1201/68,C12N15/00,G01N27/447,G01N27/447;
strandedness: Single;
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                  I30244.1 GI:605447
STS: PCR primer: STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
Homo sapiens DNA.
Homo sapiens DNA.
Eucheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eucheria; Metazoa; Catarrhini; Hominidae; Homo.

I (bases 1 to 91)
Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                Human STS UT8164, 5'
Genetic and physical mapping of simple sequence
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                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                     Matches
                                                                                                                                  Query Match
Best Local :
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rch completed: March
time: 223289 sec
                                                                               3317 GAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTG 3351
                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                    source
                                                                 71
                                                                 GAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTG
                                                                                                                                                                                                                                                                                                                                    Cycles
C 10 s
                                                                                                                     l Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 e-mail: sts@corona.med.utah.edu
Primer A: AGAGGTTGCAGTGAACCAA
Primer B: TTTTCCCCCTCTACTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted by: Utah Center for Human Genome
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                                                               Alleles:
                                                                                                                                                                                                                                                                                                                                                                          PCR Profile:
                                                                                                                                                                                                                                                                                                                                                          Initial Denaturation: 94C 300sec
                                                                                                                                                                                                                                                                                                       ycles Denaturation Annealing
10 sec. 56 C 10 sec. 70 sec. 52 C 10 sec. 72 C 20 sec. Mg++: 1.50 r
el: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                      to Label: Primer B
                                                                                                                     Conservative
                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
10. .28
                                                                                                                                                                                                   /evidence=experimental
20 c 23 g
                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1994)
             31,
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                                                                                                                                  Score 35; DB 13;
Pred. No. 9.9e-06;
                                                                                                                     Mismatches
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                                                                                                                                            Length 91;
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                                                                                                                                                                                                                                                                                                                                    Extension 30
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sec
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Page 6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             March 31, 2000, 10:14:26; Search time 599.64 Seconds (without alignments) 12517.532 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGAATATTTATAGAGTCC......GCAGTTTTCATTTGTCTGGT 30001
Inter-Alu specific Inter-Alu specific Sequence of a micr Repeat sequence fr Microsatellite seq Repeat sequence fr Repeat sequence fr Sequence of a micr Sequence of a micr Sequence of a microsatellite seq Microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence e Sequence of a microsatellite seq Poly GT enhancer e Sequence e Seq
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Alu PCR primer 2.
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Alu PCR primer 1.
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Repeat sequence fr
Repeat sequence fr
(dC-dA)n.(dG-dT)
Repeat sequence fr
Repeat sequence fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
V39744/c
TD V39744 standard; cDNA; 88
                                                  Pri detecting nucleic acids, telomerase activity, oncogene mutations, or pri cancer specific sequences, for diagnosis of disease
Example 11; Page 318; 478pp; English.

CC A process has been developed for determining the sequence of a target nucleic acid. The process comprises: (1) generating at least two concerns the process comprises: (1) generating at least two concerns the process comprises: (1) generating at least two concerns the process in v39483 to v39592 are greated to detect genetic diseases.

CC of the above process. The process is used to detect genetic diseases comprises: (2) or the above process. The process is used to detect genetic diseases. CC of the above process. The process is used to detect genetic diseases. CC of the above process. The process is used to detect genetic diseases. CC of predisposition); infections and cancers; also for establishing constity and heredity. Particular applications are diagnosis of neuroblastoma, detecting telomerase, determining family relationships constity and in genetic fingerprinting. Compared with known methods using MS, this process requires fewer specific reagents cand is better suited to automation. Extended primers are shorter; primer annealing is more efficient and the process allows detection of construction and example from the present invention.

Sequence 88 BP; 56 A; 5 C; 7 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1998.
06-NOV-1997; UZ-947801.
08-OCT-1997; US-947801.
06-NOV-1996; US-74481.
06-NOV-1996; US-74659.
06-NOV-1996; US-746036.
06-NOV-1996; US-746036.
23-JAN-1997; US-78639.
19-SEP-1997; US-933792.
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444210387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SEQU-) SEQUENOM INC.
Braun A, Damhoffer-Demar B,
Koster H, Little DP, Lough
Van Den Boom D, Xiang G;
WPI: 98-286975/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellité analysis antisense strand SEQ ID NO:262.
Mass spectrometry; diagnosis; detection; biological sample; infection; genetic disease; chromosomal abnormality; identification; heredity; pathogenic organism; telomerase activity; oncogene mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing nucleic acid by mass spectrometric analysis detecting nucleic acids, telomerase activity, oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic. W09820166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer-specific sequence; primer; ss.
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Q3373
Q33873
Q33921
T65742
T65744
T65774
T65774
T65777
T65777
T65777
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, Tang K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat sequence f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsatellite Microsatellite
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mutations,
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Minimum DB Maximum DB

seq

length: 105

length:

Post-processing: Listing first

45 summaries

N_Geneseq_36:*

Result

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Score

Query Match

Length

V3974

0 0 0 0 0 0 0

Microsatellite seq Repeat sequence Sequence of a micr

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Query Match
Best Local Similarity
Matches 63; Conserv

Conservative

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Score 63; DB Pred. No. 5.8 0; Mismatches

3 1; 5.8e-08; 0;

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Gaps

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Length 88 Indels

0.2%;

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V19045 Q33534

T6579

000000

Word size

Searched:

311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters:

Title: Perfect score:

US-08-852-495C-1_COPY_165000_195000 30001 1 AGTGAATATTTATAGAGTCC......GCAG

OM nucleic

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nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Com

Compugen Ltd

Scoring table: Sequence:

OLIGO_NUC , Gapop 60.0 ,

Gapext 60

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RESULT
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                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                          problection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols as primers placelosure; Column 11-12; 186pp; English.

Disclosure; Column 11-12; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences for invention relates to the isolation of polymorphic repeat sequences. The invention relates to the isolation of polymorphic repeat sequences can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, the invention of the invention analysis of genetic disease, containing the repeat sequences were isolated by hybridisation of containing the repeat sequences were isolated by hybridisation of probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers 765798-76647. Those clones where the repeat sequence has been determined are shown in 765704-797. This repeat sequence is from the marker clone Mdf67 which contains the repeat sequence having the formula: (TO)12(AC)18.

Sequence 60 BP; 18 A; 30 C; 0 G; 12 T;
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                          28932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21574 TCT 21576
10-DEC-1996.
21-APR-1989;
21-APR-1989;
05-SEP-1991;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1989;
21-APR-1989;
05-SEP-1991;
04-APR-1994;
                                                                                                                       Repeat sequence from polymorphic marker clone Mfd39.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfd67.
Polymorphism; repeat sequence; genetic marker; primer; amplificati
PCR; polymerase chain reaction; paternity; maternity; human; pedig
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                            US5582979-A.
                                                                                                                                                                                                               T65740 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T65762 standard; DNA; 60
                                                                                                          hybridisation; chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MARS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridisation; chromosome; ds.
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US-341562.
US-754351.
US-222177.
341562.
US-341562.
US-754351.
US-222177.
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                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     Score 54;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                 Length 60
                                                                                                                                                                                                                                                                                                                                                        Indels
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the clones
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RESULT
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DR WPI; 97-042299/04.

PT Detection of polymorphic genetic markers of the form PT Detection of polymorphic genetic acid mols. as primers PT (20 da)n(dG-dT)n - using novel nucleic acid mols. as primers PT (20 da)n(dG-dT)n which can be used as genetic CC The invention relates to the isolation of polymorphic repeat sequences CC markers. Primers based on these sequences can be used to detect these CC markers. Primers based on the sequences can be used to detect these CC markers. Primers based on the region of the sequences can be used to detect these CC commercial animal or plant breeding or pedigree analysis of genetic disease, CC commercial animal or plant breeding or pedigree analysis.

CC The repeats, when analysed, fall into 4 categories:

CC 1) perfect repeats which are alternating tandem CA repeats with no CC interruptions and without adjacent repeats of another sequence;

CC 2) imperfect repeats which are defined as 2 or more runs of uninterrupted CC 2) imperfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases;

CC 3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases from a run of at least CC 3 uninterrupted dinucleotide or longer repeats of a sequence other than CC 4) imperfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect 
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pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
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Best Local S
Matches 50
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10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
21-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MARS-)
Weber J
compound repeats except that the runs of CA are This sequence is an example of a compound imperf structure: T(CT)12GTT(TC)11T(CA)14A(AC)6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (dC-dA)n (dG-dT)n polymorphic repeat sequence #12.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
Linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T66081 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 97-042299/04
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                          interrupted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PT Detection of polymorphic genetic markers of the form
PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
PS Disclosure; Column 13-14; 186pp; English.
CC The invention relates to the isolation of polymorphic repeat sequences
CC thaving the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC comman genetic analysis such as linkage analysis of genetic disease,
CC commercial animal or plant breeding or pedigree analysis. Clones
CC containing the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC grobe. Over 100 repeat blocks were isolated by hybridisation of
CC were amplified by primers T65798-T66047. Those clones where the repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence is from the marker clone Mdfill which contains the repeat
CC sequence having the formula: (ATTT)llAT.
SQ Sequence 46 BP; 12 A; 0 C; 0 G; 34 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Best Local S
Matches 50
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Best Local
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10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
21-APR-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
US5582979-A.
10-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T65781;
                                                                                    Repeat sequence from polymorphic marker clone Mfd5.

Polymorphism; repeat sequence; genetic marker; primer; amplification;

PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                             T65707 standard;
T65707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat sequence from polymorphic marker clone Mfd110;
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                         17-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MARS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridisation; chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                              46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                   DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  0.2%;
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                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  . 46;
NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Le 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 92;
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pr detection of polymorphic genetic markers of the form
pr (dd-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
Claim 1; Column 13-14; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing,
CC human genetic analysis such as linkage analysis of genetic disease,
CC containing the repeat sequences were isolated by hybridisation of
CC containing the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC probe. Over 100 repeat blocks were isolated. The inserts from the clones
CC were amplified by primers T65798-T66047. Those clones where the repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence is from the marker clone Mdf120 which contains the repeat
CC Sequence 50 BP; 20 A; 25 C; 0 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PT Detection of polymorphic genetic markers of the form

PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols: as primers

Claim 1; Column 9-10; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences

The invention relates to the isolation of polymorphic repeat sequences

CC markers. Primers based on these sequences can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC contains the sepecially for use in e.g paternity or maternity testing,

CC commercial animal or plant breeding or peddyree analysis clones

CC containing the repeat sequences were isolated by hybridisation of

CC probe. Over 100 repeat blocks were isolated by hybridisation of

CC probe. Over 100 repeat blocks were isolated The inserts from the clones

CC were amplified by primers T65798-T66047. Those clones where the repeat

CC sequence has been determined are shown in T65704-797. This repeat

CC sequence is from the marker clone Mdf5 which contains the repeat

CC sequence 56 BP; 23 A; 28 C; 0 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1989; U
21-APR-1989; U
05-SEP-1991; U
04-APR-1994; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat sequence from polymorphic marker clone Mfd120.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MARS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T65791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARSHFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341562.
; US-341562.
; US-754351.
; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.1%;
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0.015;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                           PT gene mapping, and selective breeding

PS Table 7; Page 170; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between

CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC One out of 50 clones cross-hybridised. Assuming independent

CC distribution of microsatellites and MboI sites; the frequency of

CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,

CC 000. The sequence information for ca. 230 such bovine microsatellites

CC is summarised in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence

CC were used to generate the required PCR primers for in vitro

CC amplification of the corresp. microsatellite using the program

CC opTIPRIM). The microsatellites may be used to identify individuals,

CC for parentage testing, and in the genetic mapping of economic trait

CC loci, or genes involved the determinism of economically important

CC traits esp. in cattle, to allow selective breeding.

Sequence 56 BP; 19 A; 0 C; 28 G; 9 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 41; Conser
                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA182. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-1993 (first entry)
Microsatellite sequence from clone AGLA296.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
(GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                         W09213102-A.
06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                         Q33779 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q33603 standard; DNA; 56
                                                                                                     Bos taurus
                                                                                                                                                                              033779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - used in
                                                                                                                                                               02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5-JAN-1992; U00340
L5-JAN-1991; US-642
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nes 41; Conser
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ilarity 100.0%;
Conservative (
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                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                         0.1%;
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                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                         Score 41; DB; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                         DB 1;
0.027;
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0.028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .028;
                                                                                                                             cattle; parentage.
                                                                                                                                                                                                                                                                                                                           ç,
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                                                                                                                                                                                                                                                                                                                                                      Length 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PT Polymorphic bovine DNA markers - used in genetic identification, proceeding gene mapping, and selective breeding PS Table 7; Page 241; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by CC screening a library of bovine Mbol DNA fragments of between CC 250 and 500 by with an (AC)15 and a (TC)15 olligonucleotide probe. CC One out of 50 clones cross-hybridised. Assuming independent CC distribution of microsatellites and Mbol Sites, the frequency of CC (TS)n >9 microsatellites in the bovine genome is estimated at >100, CC is summarised in the specification and indexed herein (see below). CC The sequence supstream and downstream of the microsatellites sequence cc were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program CC amplification of the corresp. microsatellite (using the program CC amplification, and in the genetic mapping of economic trait CC icoi, or genes involved the determinism of economically important CC traits esp. in cattle, to allow selective breeding.

See also Q33501-34437.

See also Q33501-34437.

Sequence 62 BP; 22 A; 0 C; 31 G; 9 T;
                                                                                                   polymorphic bovine DNA markers - used in genetic identification,

gene mapping, and selective breeding

Table 7; Page 167; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine MboI DNA fragments of between

250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

One out of 50 clones cross-hybridised. Assuming independent

distribution of microsatellites and MboI sites, the frequency of

(T6)n >9 microsatellites in the bovine genome is estimated at >100,

000. The sequence information for ca. 230 such bovine microsatellites

is summarised in the specification and indexed herein (see below).

Stream seed to generate the required PCR primers for in vitro

amplification of the corresp. microsatellite (using the program

OPTIPRIM). The microsatellites may be used to dentify individuals,

for parentage and in the broader manning of economic testify

optimized the required pCR primers for in vitro

amplification of the corresp. microsatellite (using the program

optimized program of the microsatellites may be used to identify individuals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09213102-A.
06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone AGLA29.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q33594 standard; DNA; 63 BP Q33594;
traits esp. in cattle, to allow See also Q33501-34437. Sequence 63 BP; 22 A; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Georges M, Massey JM;
WPI; 92-284684/34.
                                                              for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.1%;
ilarity 100.0%;
Conservative (
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Pred. No.
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                                            selective breeding.
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  <u>ن</u>
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Query Match Best Local S Matches 41

Similarity

0.1%; llarity 100.0%; Conservative

%; Score 41; DB
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DB 1; 0.026;

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Pri gene mapping, and selective breeding

Rough Table 7; Page 176; 517pp; English.

Come out of a library of bovine microsatellite sequence obtd. by

Come out of 50 clones cross hybridised. Assuming independent

Come out of 50 clones cross hybridised. Assuming independent

Come out of 50 clones cross hybridised. Assuming independent

Come out of 50 clones cross hybridised. Assuming independent

Come out of 50 clones cross hybridised. Assuming independent

Compared to the sequence information for ca. 20 such bovine microsatellites

Compared to generate the specification and indexed herein (see below).

Come used to generate the required pcr primers for in vitro

complification of the corresp. microsatellites may be used to identify individuals,

Compared testing, and in the genetic mapping of economic trait

Compared testing, and in the genetic mapping of economic trait

Compared testing, and in the genetic mapping of economic trait

Compared testing, and in the genetic mapping of economic trait

Compared testing, and in the genetic mapping of economic trait

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Compared testing, and in the genetic mapping of economic trait

Compared testing 
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Best Local s
Matches 40
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15-JAN-1998.
09-JUL-1996; W0-U11478.
09-JUL-1996; WO-U11478.
(USSH) US DEPT HEALTH 6 HUMAN SERVICES.
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Georges M, Massey JM;
WPI; 92-284684/34.
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Microsatellite sequence from clone AGLA8.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
Kouprina NY, Larionov VL, Perkins EL, Resnick MA; WPI; 98-110234/10.

Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, yeast telomere and nucleic acid for recombination Example 1; Page 45; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alu PCR primer 2. PCR; primer; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V19045;
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15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces sp. W09801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V19045 standard; DNA; 40
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Similarity 100.0%;
40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; Alu repeat sequence; vector; chromosome; YAC; ss.
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Pred. No.
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0.053;
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RESULT V19044

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Matches Query Match Best Local

Local 38;

Similarity

0.1%;

Score 38; Pred. No.

DB 1; 0.15;

Length 64;

Conservative

0;

Mismatches

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Gaps

0

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V19044 standard; DNA; 40 BP V19044; 28-JUL-1998 (first entry)

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RESULT 1
Q33534/c
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           នននិនិនិនិនិនិនិ
PT Polymorphic bowine DNA markers - used in genetic identification, proper gene mapping, and selective breeding fable 7; Page 14; 517pp; English.

CC The sequence is that of a bowine microsatellite sequence obtd. by cc screening a library of bowine MboI DNA fragments of between CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe. CC One out of 50 clones cross-hybridised. Assuming independent CC (15)n >9 microsatellites and MboI sites, the frequency of CC (T6)n >9 microsatellites in the bowine genome is estimated at >100, CC (00). The sequence information for ca. 230 such bowine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence complification of the corresp. microsatellite (using the program CC opTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait CC traits esp. in cattle, to allow selective breeding.

See also Q33501-34437.

So Sequence 64 BP; 19 A; 1 C; 30 G; 14 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 9 A; 8 C; 19 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone AGLA226.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q33534 standard;
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15-JAN-1991;
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llarity 100.0%;
Conservative
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Pred. No.
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RESULT 15
V19044/c
ID V19044;
AC V19044;
DT 28-JUL-1998 (first entry)
DE Alu PCR primer 1.
KW PCR; primer; amplification,
KW circular yeast artificial (
OS Synthetic.
OS Saccharomyces sp.
PN W09801573-A1.
PD 15-JAN-1998; WO-U11478.
PR (09-JUL-1996; WO-U11478.
PR (1934) US DEPT HEALTH & HI
PI KOUPFINA MY, LAFIONOV VL, 1
DR WPI; 98-110234/10.
PT Preparation of yeast artif.
PT recombination using vector
PT yeast telomeare and nuclecic
PS Example 1; Page 45; 117pp;
CC This is the nucleotide seq
CC amplification of the Alu r.
CC demonstrate the processes of city of the creation and use of city to selectively clone specific to selectively clone specific mixed nucleic acids by int CC They can be used to rapidl Sequence of DNA is known.
CC be easily cloned and analy Sequence 40 BP; 7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, preparation using vector comprising yeast tentromere, marker, preparation using vector comprising yeast tentromere, marker, preparation using vector comprising yeast tentromere and nucleic acid for recombination Example 1: Page 45; 117pp; English.

Example 1: Page 45; 117pp; English.

Camplification of the Alu repeat sequence, which is used in the camplification of the Alu repeat sequence, which is used to comprise the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of the sequence of DNA is known. Using the vector(s) into E. coli cells. Campled to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

So Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
                                                                                                                             Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination Example 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.
    Query Match 0.1
Best Local Similarity 100
Matches 36; Conservative
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Best Local Similarity
Matches 36; Conserv
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PCR; primer; amplification; Alu repeat sequence;
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100.0%; Pr
175 0;
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7 A; 12
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VL, Perkins EL, Re
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    Score 36; DB; Pred. No. 0.5
0; Mismatches
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37
           GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCAC
GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCAC
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Saccharomyces sp.
W09801573-A1.
15-JAN-1998.
09-JUL-1996; U11478.
09-JUL-1996; W0-U11478.
09-JUL-1996; W0-U11478.
(USSH) US DEPP HEALTH & HU
KOUPTINA NY, LATIONOV VL, F

& HUMAN SERVICES

Perkins EL,

Resnick MA;

Alu PCR primer 1.

PCR; primer; amplification; Alu repeat sequence; circular yeast artificial chromosome; YAC; ss.

Synthetic

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Perfect score:
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
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Match
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-222-177A-322

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US-08-222-177A-317

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US-08-222-177A-104
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US-08-222-177A-166
US-08-222-177A-430
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US-08-222-177A-244
                                                ; IMMEDIATE SOURCE:
; CLONE: mfd67rs
US-08-222-177A-244
 Query Match
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APPLICANT: Weber,
                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                  TOPOLOGY:
                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                            TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
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ALIGNMENTS	08-222	-08-222	-08-222	-08-222-177A	08-222	08-222	08-222	08-222	-08-222	08-222	08-222	-08-222	08-222	3-08-222	08-222	08-222	S-08-222	:-08-222	-08-222
MENTS	-08-222-177A-101	-222-177A-364	-222-177A-203	2-177A-157	-08-222-177A-249	-08-222-177A-241	-08-222-177A-195	2-177A-388	-222-177A-370	2-177A-229	1-08-222-177A-53	-222-177A-232	-08-222-177A-183	-222-177A-74	-08-222-177A-403	-08-222-177A-400	-222-177A-119	-222-177A-137	222-177A-397
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/341
FILING DATE: 21 APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-210
                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                    TYPE: nucleic acid
                                                                                                                                                     TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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5. 5582979
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NVENTION: LENGTH POLYMORPHISMS IN
NVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
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8000 Excelsior Drive, Suite 401
DNA (genomic)
                                        double
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                                                                                                     RESULT
                                        Sequence 430, Application US/08222177A Patent No. 5582979
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 09.492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
APPLICANT: Weber, James L. TITLE OF INVENTION: LENGTH TITLE OF INVENTION: (dC-dA
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CLONE: mfd39rs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                       0.2%;
LENGTH POLYMORPHISMS IN (dC-dA)n. (dG-dT)n SEQUENCES AND METHODS OF USING SAME
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Pred. No.
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Best Local S
Matches 50
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                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
THY FUNDAME: 1200 031-1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 92 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ro
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                            STREET:
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CLASSIFICATION: 435
IOR APPLICATION DATA:
                                FILING DATE:
                                                 APPLICATION NUMBER:
                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                             CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                          53717-1914
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8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                              E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
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                                                                                                                                                                                          USA
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                                                   US/08/222,177A
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US 07/341,562 FILING DATE: 21-APR-1989

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; Sequence 65, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atent No. 5582979
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: SATA, Chartes 30,492
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09f
TELECOMMUNICATION INFORMATION:
TFLEPHONE: (608) 831-2100
                                                                                                                         NAME: Sara, Charles S. REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: mfd110rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weber, James TITLE OF INVENTION: LENC TITLE OF INVENTION: (dC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Madison
STATE: Wisconsin
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: 11
                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (608) 831-2106
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 STRANDEDNESS:
                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
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5582979
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              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                             56 base pairs
                                                                                             (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                            (808)
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double
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                                                                                                            831-2100
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LENGTH POLYMORPHISMS IN
(dC-dA)n.(dG-dT)n SEQUENCES AND METHODS
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100.0%; Pred. No. 3.9e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                      US 07/341,562
                                                                                                                                                                                                                                                                                   US/08/222,177A
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RESULT

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Best Local Similarity
Matches 42; Conserve
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;; IMMEDIATE SOURCE:
; CLONE: mfd5rs
US-08-222-177A-65
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                                                        Query Match
Best Local S
Matches 41
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                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SAIB, CDAT1es S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA IMMEDIATE SOURCE: CLONE: mfd120rs
                           COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: LENGTH
TITLE OF INVENTION: (dC-da
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
                                                        / Match 0.1%; So Local Similarity 100.0%; local Similarity 100.0%; les 41; Conservative 0;
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                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                                                            (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                              US 07/341,562
                                                                                                                                                                                                                                                                379:
                                                                                                                                                                                                                                                                                                                                        09865.601
                                                        Score 41; DB; Pred. No. 0. 0. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
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                                                   DB 1;
o. 0.00015;
o. 0;
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                                                                                     Length 50;
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                                                        Gaps
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RESULT 8
US-08-222-177A-175
; Sequence 175, Application US/08222177A
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Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                  Patent No. 5582979
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                           28944 CTCTCTCTCACACACACACACACACACACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 091
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                          APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n.(dg-dT)n SEQUEN
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: mfd97rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/222,177A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                       ADDRESSEE:
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                    53717-1914
                                                                      Madison
READABLE FORM
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                                                 Wisconsin
                                                                                      E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                            (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                              0.1%; Score 33;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/341,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,492
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Query Match
Best Local Similarity
Matches 33; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7:
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28954 CACACACACACACACACACACACACACACAT 28986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNI IMMEDIATE SOURCE: CLONE: mfd42rs
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin KET CURRENT APPLICATION NUMBER: US
                                                   FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                   REGISTRATION NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                         CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CACACACACACACACACACACACACACACAT 33
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o. 5582979
                                                                                                                                                                                                                                                                                                                                 53717-1914
                                                                                                                                                                                                                                                                                                                                                                     Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                           8000 Excelsior Drive, Suite 401
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0.054;
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US-08-222-177A-317
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                                                                                  US-08-222-177A-317
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Query Match 0.1%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 0. Matches 33; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
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SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNF IMMEDIATE SOURCE: CLONE: mfd99rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/222,177A
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 33; Conserva
                                                                                                                                                              STRANDEDNESS:
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53717-1914
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(608) 831-2106
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0.052;
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GENEAUT: Orr, Harry 1.

APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: 20ghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
PATENT NO. 5741645
FATHLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 NO. 5741645th Fourth Street, Suite 203
                                                                       Sequence 45, Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: OTI, Harry T.
APPLICANT: Ranum, Laura P. M.
APPLICANT: Cohung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for the sequence of the sequence 
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US-08-469-802B-27
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US-08-267-803B-45
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
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MEDIUM TYPE: Floppy
ent No. 5834183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 55401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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5, 5741645
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Type 1 and Method for Diagnosis
                                                                                     Gene Sequence for Spinocerebellar Ataxia
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LENGTH: 62
5506118-3
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5506118-3/c
; PATENT NO. 5506118
; PAPPLICANT: BERG, DAVID T.; GRINNELL, BRIAN W.
; TITLE OF INVENTION: METHOD OF USING EUKARYOTIC EXPRESSION
; VECTORS COMPRISING A POLY GT ELEMENT IN THE PRESENCE OF
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                                                                                                                                                                                                  FILING DATE: 07-OCT-1988 SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                   TRANS-ACTING GENE PRODUCTS NUMBER OF SEQUENCES: 1
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Best Local S
Matches 33
                                                                                      Query Match
Best Local Similarity
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                                28953 TCACACACACACACACACACACACACACACA 28985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MCCOrmack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1228
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,475
FILING DATE: 23-AUG-1993
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 54 base pairs
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CORRESPONDENCE ADDRESSE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
                                                                                                                                                                                                                                       FILING DATE: 15-JUL-1992
APPLICATION NUMBER: 255,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/267,803B FILING DATE: 28-JUN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 914,651
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TCACACACACACACACACACACACACACACA 21
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                                                                    0.1%; Score 33;
100.0%; Pred. No.
tive 0; Mismatc
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100.0%; Pred. No. 0.051;
tive 0; Mismatches
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0.05;
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US-08-222-177A-218
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US-08-222-177A-59
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                                                                                                                                                                                       Sequence 218, Application US/08222177A Patent No. 5582979
GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linea:
MOLECULE TYPE: DN
IMMEDIATE SOURCE:
CLONE: mfd3rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/341,562
FILING DATE: 21-APR-1989
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TITLE OF INVENTION: (d
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
                                                                                                                      APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-dA)n.(dg-dT)n SEQUENCES
NUMBER OF SEQUENCES: 460
                                                                                                     CORRESPONDENCE ADDRESS:
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XY: USA
53717-1914
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                               Wisconsin
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8000 Excelsior Drive, Suite 401
                                                                  E: DeWitt Ross
8000 Excelsion
                                                                                                                                                                                                                                                                                                                                                                                            0.1%; Score 32; DB 1; llarity 100.0%; Pred. No. 0.12; Conservative 0; Mismatches
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                                                                    & Stevens, S.C.
Drive, Suite 401
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COMPUTER READABLE FORM:

MEDITH TYPE: Flopy disk
COMPUTER: IDM C Commattly
COMPUTER: IDM C Commattly
COMPUTER: Patentin Release #1.0, version #1.25

CURENTING SYSTEM: PC DOS/MS-DOS
CURENT APPLICATION NUMBER: US 07/341.562

APPLICATION NUMBER: US 07/341.562

APPLICATION NUMBER: US 07/341.562

APPLICATION NUMBER: US 07/341.562

APPLICATION NUMBER: 30.492
APPLICATION NUMBER: 30.492
APPLICATION NUMBER: 09865.601

FILING DATE: 21-ARR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
APPLICATION NUMBER: 30.492
REFERENCE/DOCKET NUMBER: 09865.601

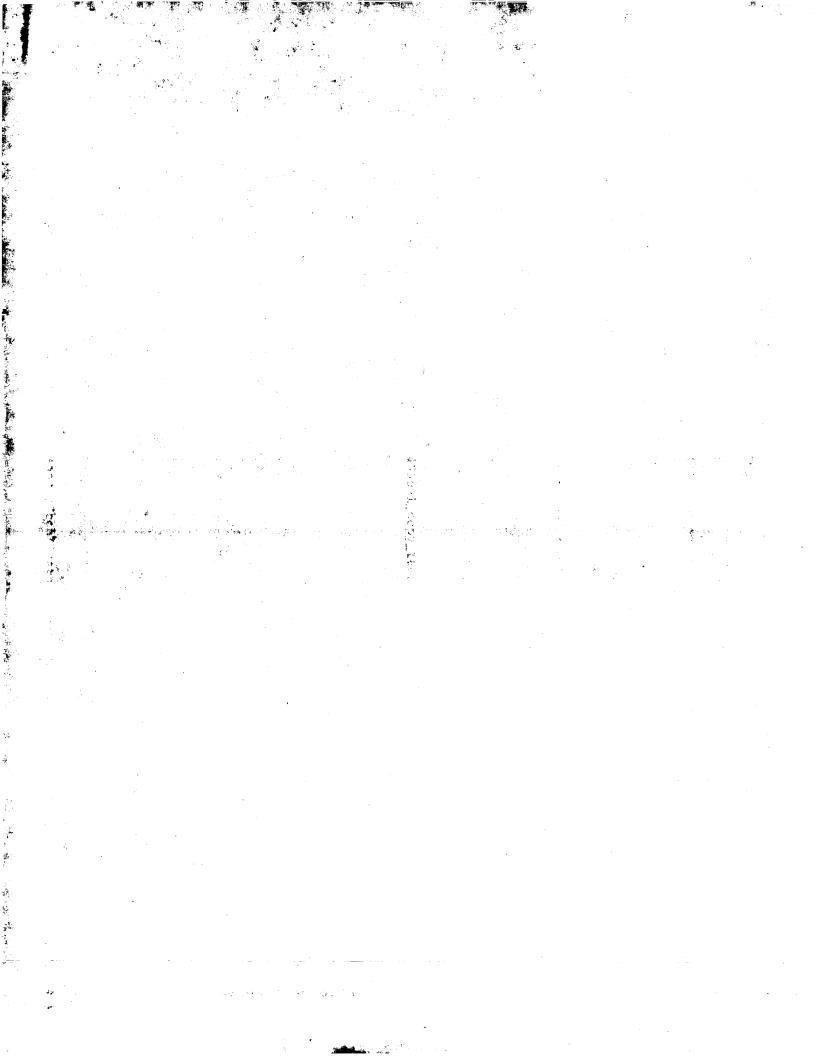
FILING DATE: 21-ARR-1989
ATTORNATION: 608) 831-2100

TELEPONE: (608) 831-2100

TELEPONE: (608) 831-2106

TELEPONE: (608) 831-2106

TELEPA: (608) 831-2
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Title: Perfect score: Sequence:

Scoring table:

OM nucleic -

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13847.741 Million cell updates/sec
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N68192
N68192.1
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zallf07.sl Soares fetal
IMAGE:292261 3' similar
                                                                                                                                                                                                                                                                                                                      Unpublished (1995)
On Apr 14, 1993 this sequence version replaced Contact: Wilson RK
Washington University School of Medicine
                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalli
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 75)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                            The WashU-Merck EST Project
                                                       Wilson, R.
                                                                                                                                           Homo sapiens
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AA053038
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AA14458 mrsu...
AA515337 ng71c01.s
B47960 RPCI11-3M4.
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A1040422 Homo sapi
A1045154 Homo sapi
B03985 cSRL-2155-u
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AQ025047 EP(2)1183
A1569475 tn87e04.x
AA289455 vb36612.r
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AA916300 on22c08.s
AA983697 on59f10.s
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C05051 C05051 Huma
AA548135 nx55811.s
B80126 CIT-HSP-204
AA9276139 CITB-E1-
AA578401 n153c01.s
AQ276139 CITB-E1-
AA578401 n153c01.s
AQ276139 CITB-E2-
AA578401 n53c01.s
AQ276139 CITB-20-
AA598425 CIT-HSP-204
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AA959576 ze61h02.s
AA959576 ze61h02.s
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                       g1:503479
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AA078242 7H16G05 C
AA500598 vi90a02.r
B37890 HS-1046-A2-
R67088 yi30h05.s1
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AW099072 sd33h06.

AP988425 oq95912.

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AA595747 nj28e09.

AA019576 ze61h02.

AA019576 ze61h02.
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T25653 EST00522
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D20989 HUMGS01971
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AA053038 z171e12.s
                                                                                       Marra, M.,
                                                                                                                                  Mammalia;
                                                                                                                                                                                                                      clone
                                                        REFERENCE
AUTHORS
TITLE
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B62983/c
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Best Local S
Matches 45
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                      source
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Contact: Ung-Jin Kim
Callech Genome Research L
California Institute of T
Division of Biology, MS 1
Tel: 626 796 7066
Fax: 626 395 4901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: mis two words of the High quality sequence stop: 61.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq.primer: ml3 -40 forward
Seq.primer: ml3 -40 forward
                                                                                                                                                                                                                    Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 102)
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B62983
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CIT-HSP-669F15.TP CIT-HSP
                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                      Email: ung@ash.tree.caltech.edu
Clones are available from Research
                                                                                                                                                                                               Kim, U.-J., Adams, M.D. and Simon, M.I.
Determination of clone end sequences
                                                                                                                                                                                                                                                      Homo sapiens
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/db_xref="GDB:3800034"
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/clone="IMAGE:292261"
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/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
  /organism-"Homo sapiens"
/db_xref-"GDB:5491647"
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                                                                                                                                 Technology
147-75, Pasadena,
                                                                                                                                                                                                                                                                                                                      Homo
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0.0016;
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Best Local
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                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA053038 91 bp mrna
z171e12.s1 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:510094 3' similar to contains Alu repetitive element;, 1
                                                                                                                                                                                                                                                                   Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiapee, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hultman, M., Kucaba, T., Laey, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Mohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Conservative
                                                                                                                                                                                                                                                          IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40M13 fwd. from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                        On May 18, 1995 this sequence version Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA053038.1
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               16
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          /db_xref="taxon:9606"
/clone="669F15"
                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:510094"
                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:3813427"
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type-"Sperm"
/note-"Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.1%;
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Pred. No.
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0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                        replaced
                                                                                                                                                                                                                                                                                                                                                           Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                              adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                        g1:811133.
                                                                                               Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
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T25653/c
                                                                                                                                                                                           BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
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MEDLINE
                                                                                                              Matches
                                                 70
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Query Match

0.18;

Score 44;

BB 27;

Length

91;

DEFINITION

brain 1NIB Homo

sapiens cDNA clone

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RESULT
R18531/c
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ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100 Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29813 GAGGTGGAGGTTGCAGTGAGCCGAGATGGCGCCACTGCACTCCA 29856
                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 GAGGTGGAGGTTGCAGTGAGCCGAGATGGCGCCACTGCACTCCA 4
                                                                                                                         T25653
EST00522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus
T25653
R18531 96
yf96e06.rl Soares
                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T25653.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wayne State University
5047 Gullen Mall, Detroit, MI
Tel: 3135776708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Ko MSH
Center for Molecular Medicine and Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 93)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msko@cmb.biosci.wayne.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KO, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eic Acids Res.
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                     /note="vector: pBluescript SK(-); Site_1: NotI; Site_2: ECORI; mRNA was purified from the mouse Ltk- fibroblastoid cultured cells. Double-stranded cDNAs were synthesized from the mRNA using an oligo(dT) NotI primer. After shearing to 200-400 bp, a synthetic linker-primer, which has one blunt and one sticky end and internal EcoRI site, was ligated to the cDNAs. The cDNAs were amplified by the polymerase chain reaction (PCR) using the ligated linker-primer sequence. After denaturation and reassociation of the ds-cDNAs, and isolation of single-stranded cDNAs were again amplified by PCR. The cDNAs were digested with EcoRI and NotI, and inserted into a plasmid vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 bp mRNA EST 31-OCT-199 Equalized cDNA library from Ltk- cultured cells Mus cDNA cione A0001D11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Equalized cDNA library from Ltk- cultured cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="A0001D11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:562974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain-"C3H/An"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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infant
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                                                                                                                                                                                                   Score 43; DB 20;
; Pred. No. 0.0057;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                         Length 93;
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TITLE
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AUTHORS
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ORGANISM
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VERSION
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AA129957
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ORIGIN
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KEYWORDS
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            SOURCE
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Best Local S
Matches 42
ORGANISM
                                                                                                                                                                                          source
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R18531.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 96)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., and Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                       sequence.
AA129957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu

Insert Size: 2194

Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read Insert Length: 2194 Std Error: 0.00
                                                                                     zn86h04.rl Stratagene lung
IMAGE:565111 5' similar to
                                                                                                                                                                                                                                                       l Similarity
42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson, R.
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                                                                                                                   AA129957
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Homo sapiens
                               EST
                                         AA129957.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13RP1
               man
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Location/Qualifiers
                                                                                                                                                                                                                                                     0.1%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:30391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="Soares infant brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:402738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1995)
                                                                                                                   104 bp
                                                                                                                                                                                                                                                     Score 42; DB 21; 
pred. No. 0.011; 
0; Mismatches
                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contains Alu repetitive element; contains mRNA sequence.
                                                                                       carcinoma contains !
                                                                                     EST 27-NOV-199 a 937218 Homo sapiens cDN Alu repetitive element;
                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Louis,
                                                                                                                                                                                                                                                                                   Length 96;
                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                       0;
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ed with a Not
                                                                                                     cDNA clone
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                       0.
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VERSION
KEYWORDS
                                                           REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                        RESULT
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MEDLINE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                     EST
                                                                                                                                     human
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TGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGC 90
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1 (bases 1 to 104)

Hillier L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., HavKins, M., Hultman, M., Kucaba, T., Lacy, M., J., Prange, C., Rifkin, L., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Travaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
Eutherla; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 95)

1 (lases 1 to 95)

1 (lases 1 to 95)

1 (lases 1 to 95)

2 (lases 1 to 95)

3 (lases 1 to 95)

4 (lases 1 to 95)

5 (lases 1 to 95)

5 (lases 1 to 95)

6 (lases 1 to 95)

8 (lases 1 to 95)

9 (lases 1 to 95)

8 (lases 1 to 95)

9 (lases 1 to 95)

9 (lases 1 to 95)

1 (lases 1 to 95)

2 (lases 1 to 95)

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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 92.
Location/Qualifiers
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Genome Res. 6 (9), 807–828 (1996)
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11; Conservative
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/clone="IMAGE:565111"
/clone_1ib="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
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/db_xref="GDB:4594175"
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MEDLINE
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yc21f01.s1 Stratagene lung (#93/21v
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Email: est@watson.wustl.edu
Insert Size: 513
Insert Size: 513
High qality sequence stops: 69 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                   Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Le,
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Fax: 314 286 1810
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On Nov 6, 1997 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)
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                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807–828 (1996)
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/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI.
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
Total ovary; tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
GACTCGAGTTTTTTTTTTTTTTTTTT 3'"

CTCGAGTTTTTTTTTTTTTTTTTT 3'"

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/clone_lib="Stratagene ovary (#937217)"
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on22c08.sl
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On May 5, 1995 this sequence version replaced gi:797742.
On May 5, 1995 this sequence version replaced gi:797742.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Email: Robert Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., 1
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Seg primer: -21m13
                                                                                                                                                                                                            CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Chri. Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anat
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1557422"
/clone=!b="NCI_CGAP_Lu5"
/tlssue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:81337"
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/db_xref="GDB:484954"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene lung (#937210)"
        'note="Organ: lung; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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NCI_CGAP_Lu5
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Pred. No.
                                                                                                                                                                                                                                                                                                 Std Error: 0.00
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Homo sapiens cDNA clone IMAGE:1557422
repetitive element;, mRNA sequence.
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0.043;
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        pT7T3D-Pac
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(Pharmacia) with

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AA583697/c
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Best Local S
Matches 39
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 CACCTCCCGGGTTCAAGCAATTCTCCTGCCTCAGCCTCC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA583697 101 bp mRNA 26-SEP-1997 nn58f10.sl NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1088107 similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:692709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40m13 fwd. ET from Amersham
H1gh quality sequence stop: 93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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ilarity 100.0%;
Conservative
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                                                                                                                21
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                                                                                                         /note="Organ: kidney; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGGCAGGG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb. a 29 c 28 g 23 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinold, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " a 34 c 21 g 22 t
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1088107"
                                                                                                                                                                                                                                                 /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                          'sex="mixed"
                                                                                                                                                                                                                                                                                                                 clone_lib="NCI_CGAP_Kid6"
                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                     tissue_type="kidney tumor"
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  0.1%;
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mismatches
  Score 39;
Pred. No.
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0.092;
    DB 35;
0.087;
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                         Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center information can be
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N98204/c
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C05051/c
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                                                                                                                                                                                                                                             21527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                           ATTTATTTATTTATTTATTTATTTATTTATTTATTTTT 21564
                                                                                                                                                                                                      ATTTATTTATTTATTTATTTATTTATTTATTTTTT
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                                       C05051 Hum
C05051 Hum
3NHC4544,
C05051
                                                                                                                                                                                                                                                                                    38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N98204 94 bp mRNA 0288C3 czapPFDd2.1, Debopam Cclone PF0288C, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
University of Central Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium 1 (bases 1 to 94)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malaria parasite P.
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                                                                                                                                                                                                                                                                                  0.1%; So illarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                        49
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                                                                                Human heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dchak@pegasus.cc.ucf.edu
                                                                                                                                                                                                                                                                                                                                                                                                  using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDDN, and it was digested with Xho I. Prepared fragments were ligated into EcoR I + Xho I digested lambda ZAP II vector. "

A C 6 g 31 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_llb="czapPFDd2.1, Debopam Chakrabarti"
/lab_host="E. coli XL-1 blue"
/note="Vector: Lambda ZAP II; Site_1: EcoR I; Site_2: Xho
I; PolyA+ RNA, from asynchronous blood stage parasites of
I; PolyA+ RNA, from asynchronous blood stage transcribed
the Dd2 isolate cultured in vitro, was reverse transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5833"
/clone="PF0288C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1995 this sequence version replaced g1:797974
                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Debopam Chakrabarti Plasmodium falciparum
                                                                                                                                                                                                                                                                                                   Score 38; Pred. No.
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0.18;
                                                                                Homo
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RESULT 13
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Best Local
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                                                                                            Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397885.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Construction of a normalized directionally cloned cDNA library adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 104)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA548135 92 bp
nk55all.sl NCI_CGAP_Pr7
sequence.
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Tel: 81-3-5449-5372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Tokyo
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                                                                              www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute of Medical Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="3NH4444"
/clone_lib="Human heart cDNA (YNakamura)"
/dev_stage="adult"
/note="Organ: heart; normalized directionally cloned cDNA from adult heart"
26 c 37 g 17 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Homo sapiens cDNA clone IMAGE:1017404,
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B80126/c
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Best Local Similarity 100.0%;
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2042J24.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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B80126
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CIT-HSP-2042J24.TR CIT-HSP
                                                                                                                                                                                                                                                                                            Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                  end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                    Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 102)
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a 32 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .92
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1017404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:2867149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Pr7"
/sex="male"
                                                                                    /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="low-grade prostatic neoplasia"
/lab_host="DH10B"
                                                                                                                                        /sex="Male"
                                                                                                                                                                              /db_xref="taxon:9606"
/clone="2042J24"
                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:7053555"
                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                            'clone_lib="CIT-HSP"
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Best Local Similarity
Matches 37; Conser
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Best Local Similarity
Matches 37; Conserv
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                                   19898 CTGAGGCAGGAGAATCACTTGAACCCAGGAGGCAGAG 19934
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 57
Email: estéwatson.wustl.edu
Insert Size: 614
High quality sequence stops: 70 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE.
Consortium (info@image.llnl.gov) for further information.
Insert Length: 614 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 70.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105)
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ye35b02.rl Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:119691 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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                                                                                                                                                                                         b
                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:487980"
/db_xref="taxon:9606"
/clone="IMAGE:119691"
                                                                                                                                                                                                                                                                                                                                                                clone_lib="Stratagene lung (#937210)"
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Pred. No. 0.34;
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                                                                                      Homo sapiens 4000 year old 1
L36836
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Birmingham, AL 35294, US
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Oh,Y. and Warnock,D.G.
An Alu cassette in the human
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                         Homo sapiens (individual_isolate 4000 Nekht-ankh) liver DNA.
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Oh, Y. and Warnock, D.G.
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Ancient DNA: extraction, characterization, molecular cloning, enzymatic amplification
Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
89184542
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17 c 21 g
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/isolate="4000 year old
/db_xref="taxon:9606"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                             /organism-"unknown"
28 c 0 g
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                                                                                                                         GI:1822258
                                                                                                                                              50 bp DNA from patent US 5582979.
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1.3e-09;
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A68621/c
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                                                                                                                                                                                                                                                                                                                                               40
                                                                                                   unclassified.

1 (bases 1 to 85)

Jeffreys,A.J. and Armour,J.

IDENTIFICATION OF SIMPLE TANDEM REPEATS
PAtent: WO 9517522-A 44 29-JUN-1995;
UNIV LEICESTER (GB)
Other publication AU 1277995 950710.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
                                                                                                                                                                                                                                                                                                                                                                                            ch 0.1%; Score 40; DB 5; Lot 1 Similarity 100.0%; Pred. No. 1.4e-08; 40; Conservative 0; Mismatches 0;
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Sequence 1 from Patent WO9801573.
A68621 GI:4759648
                                                                                                                                                                                                                                              A45374.1
                                                                                                                                                                                                                                                         A45374 85 bp DNA
Sequence 44 from Patent WO9517522.
A45374
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Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and TRANSFORMATION ASSOCIATED RECOMBINATION CLONING Patent: WO 9801573-A 15-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unclassified
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25 c 0 g
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/db_xref="taxon:32644"
12 c 13 g
                                                                         /db_xref="taxon:32644"
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                                                                                     organism="unidentified"
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  Score 40;
Pred. No.
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   DB 5; L
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HSWG3B103/c
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                                                                                                                                                 Armour, J.A.L.

Direct Submission
Submitted (04-MAY-1995) J.A.L. Armour, University
Dept of Genetics, University Road, Leicester LEI 7

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   H.sapiens simple tandem X86915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 85)
Jeffreys, A. John and Armour, J
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AR061179
AR061179.1 GI:59
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Unclassified.
        40;
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Patent: US 5843647-A 44 01-DEC-1998;
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        similarity 100
40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
1 c 24 g
                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="wg3b10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                    /rpt_type=TANDEM
1 c 24 g
                                                                                         'note="simple tandem repeats"
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     0.1%; >--
100.0%; Pr
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patent
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        score 40; DB; pred. No. 1.3
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3' region.
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Sequence 57
AR051487
AR051487.1
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AR051499
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1 (bases 1 to 60)
de la Monte, S. and Wands, J.R.
Human alpha-galactosidase M36133 M36133.1 GI:179543
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
37; Conserv
                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 76)

de la Monte, S. and Wands, J.R.

Neural thread protein gene expression
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14 c 15 g
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19 c 18 g
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                                                           Query Match 0.1%; Score 36; DB 10; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                     Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Bernard,O.A., Romana,S.P., Schichman,S.A., Mauchauffe,M.,
Jonveaux,P. and Berger,R.

Partial duplication of HRX in acute leukemia with trisomy 11

Leukemia 9 (9), 1487-1490 (1995)

95387660

2-2-2-1 (taff at the National Library of Medicine created thi
                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 170933] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
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J. Biol. Chem. 265, 9319-9326 (1990)
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Kornreich, R. Bishop, D.F. and Desnick, R.J.
Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fabry disease; breakpoint junction; glycosphingclipid catabolism Human DNA.
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/db_xref="taxon:9606"
28 c 17 g 1
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/db_xref="taxon:9606"
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100.0%; Pred. No. 1.4e-06;
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Search completed: April 1, 2000, 01:57:28 Job time: 253997 sec

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12517.949 Million cell updates/sec
   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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PCR amplification
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RESULT T65740 ID T6 AC T6 DT 17 DE R6 KW PC

765740 standard; DNA; 91 BP.
765740;
17-JUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd39.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

B 8

X m O	SCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ი იიიიიი ი
Query Match Best Local Matches 5	762 765762 standard; D 765762; standard; D 765762; requence fr Folymorphism; repe- PCR; polymerase ch 11hdege analysis; hybridisation; chr Homo sapiens. US5582979-A. 10-DEC 1996; 21-APR-1989; US-35; 04-APR-1991; US-75; 04-APR-1991; US-75; 04-APR-1996; US-75; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 04-APR-1996; 0	335 335 337 338 338 338 338 338 338
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vat	T 1 755762 standard; DNA; 60 BP. 765762; 765762; 77677762; 776777762; 77677762; 776777762; 77677762; 776777762; 776777762; 776777762; 776777762; 776777762; 776777762; 776777762; 776777762; 776777762; 7767777762; 7767777762; 7767777777777	00000000000
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0%; Pred. No. 1.7e-08 0; Mismatches	ALIGNMENTS 17. JUN-1997 (first entry) Repeat sequence from polymorphic marker clone Mfd67. Polymorphism: repeat sequence; genetic marker; primer; amplificat PCR; polymorphism: repeat sequence; genetic marker; primer; amplificat PCR; polymorphism: repeat sequence; genetic marker; primer; amplificat PCR; polymorphism: pedilinkage analysis; genetic disease; animal; plant; breeding; locus hybridisation; chromosome; ds. 10. PDC-1996. 10. PDC-1996. 11. PRR-1989; US-341562. 12. ARR-1989; US-341562. 13. ARR-1989; US-341562. 14. ARR-1989; US-322177. 16. ARRS-) MARRHFIELD CLINIC. Weber JL; Weber	Q34053 Q34053 Q34155 Q34155 Q34155 Q34156 Q34140 Q33936 Q33936 Q34009 Q34009 Q34009 Q34009 Q34009 Q34009 Q34009 Q34009 Q34009 Q34009
Length 60; 3;); Indels 0; Gaps 0;	ALIGNMENTS Alignmently Alignm	Poly GT enhancer e Microsatellite seg Sequence of a micr Sequence of a micr Sequence of a micr Microsatellite seg Allelic ladder, Dl Microsatellite seg Sequence of a micr Repeat sequence fr Repeat sequence fr Microsatellite seg

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RESULT
T66081
         pr Detection of polymorphic genetic markers of the form pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols as primers pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols as primers pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols as primers primers has primers primers based on the isolation of polymorphic repeat sequences CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic CC markers. Primers based on these sequences can be used to detect these CC markers. Primers based on these sequences can be used to detect these CC containing the repeat breeding or paternity or maternity testing, CC containing the repeat sequences were isolated by hybridisation of CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) CC containing the repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat CC sequence has been determined are shown in T65704-797. This repeat CC sequence is from the formula: (TC)12.5GTT(TC)11.5(CA)14A(CA)5.5.
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Best Local S
Matches 50
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21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
WPI; 97-042299/04.

WPI; 97-042299/04.

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Example 8; Column 57-58; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis.

The repeats, when analysed, fall into 4 categories:

1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence;

2) imperfect repeats which are defined as 2 or more runs of uninterrupted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
US5582979-A.
10-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-1997 (first entry) (dC-dA)n.(dG-dT)n polymorphic repeat sequence #12. (dC-dA)n.(dG-dT)n polymorphic repeat sequence; penetic marker; primer; amplification; Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                          Weber
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hybridisation; ch
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50; Conserv
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chromosome;
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Pred. No.
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2.9e-07;
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RESULT T65791 ID TO AC TO

T65791 standard; DNA; T65791;

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Matches Query Match Best Local

42;

Conservative

0;

Score 42; DB Pred. No. 0.0 0; Mismatches

DB 1; L 0.00012;

Length

0

Indels

0

Gaps

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Similarity

0.1%;

42

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PT Detection of polymorphic genetic markers of the form
pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
ps Claim 1; Column 9-10; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences
CC thaving the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC commarkers. Primers based on these sequences can be used to detect these
CC containing the repeat sequences analysis of genetic disease,
CC containing the repeat sequences were isolated by hybridisation of
CC containing the repeat sequences were isolated by hybridisation of
CC containing the repeat blocks were isolated. The inserts from the clones
CC were amplified by primers T65798-T66047. Those clones where the repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence is from the marker clone Mdf5 which contains the repeat
CC sequence is from the marker clone Mdf5 which contains the repeat
CC sequence having the formula: (CT)7(CA)23.
SO Sequence 56 BP; 23 A; 28 C; 0 G; 5 T;
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Best Local :
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21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754551.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA repeats separated by no more than 3 consecutive non-repeat bases; 3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat seriom a run of at least 5 uninterrupted dinucleotide or longer repeats of a sequence other than (dC-dA)n.(dG-dT)n, or from at least 10 uninterrupted mononucleotides; and 4) imperfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect This sequence is an example of a compound imperfect repeat sequence of structure: T(CT)12GTT(TC)11T(CA)14A(AC)6.

Sequence 92 BP; 21 A; 43 C; 1 G; 27 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfd5.
Polymorphism; repeat sequence; genetic marker; primer; amplificati
PCR; polymerase chain reaction; paternity; maternity; human; pedig
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hybridisation; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                               WPI; 97-042299/04.
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50; Conservative
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pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
Claim 1; Column 13-14; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences
The invention relates to the isolation of polymorphic repeat sequences
Chaving the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
C markers. Primers based on these sequences can be used to detect these
C repeats, especially for use in e.g paternity or maternity testing,
C human genetic analysis such as linkage analysis of genetic disease,
C commercial animal or plant breeding or pedigree analysis. Clones
C containing the repeat sequences were isolated by hybridisation of
C chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
probe. Over 100 repeat blocks were isolated. The inserts from the clones
were amplified by primers 765798-766047. Those clones where the repeat
C sequence has been determined are shown in 765704-797. This repeat
C sequence is from the marker clone Mdf120 which contains the repeat
C sequence 1s from the formula: (TC)5(AC)20.
Sequence 50 BP; 20 A; 25 C; 0 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
gene mapping, and selective breeding
Table 7; Page 170; 517pp; English.
The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between
250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
one out of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and MboI sites, the frequency of
(T6)n >9 microsatellites in the bovine genome is estimated at >100,
000. The sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).
The sequences upstream and downstream of the microsatellite sequence
were used to generate the required PCR primers for in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                (GENM-) GENMARK.
GEORIGES M, MASSEY JM;
WPI; 92-284684/34.
Polymorphic bovine DNA markers - used in
                                                                                                                                                                                                                                                                                                         06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB 1993 (first entry)
Microsatellite sequence from clone AGLA296.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3/c
Q33603 standard; DNA; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism; repeat sequence; genetic marker; primer; amplificati PCR; polymerase chain reaction; paternity; maternity; human; pediglinkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat sequence from polymorphic marker clone Mfd120
                                                                                                                                                                                                                                                                                                                                                                     WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; L
0.00025;
                                                                                                                                                                                                                                    genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                             cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pedigree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT
Q33594/c
ID Q335
AC Q335
DT 02-F
DE Micr
KW PCR;
KW gene
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                                                                                                                                                                                                                                                                                                     PI Georges M, Massey JM;

PR Holymorphic bovine DNA markers - used in genetic identification,

PR Polymorphic bovine DNA markers - used in genetic identification,

PR Polymorphic bovine DNA markers - used in genetic identification,

PR page 241; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between

CC One out of 50 clones cross-hybridised. Assuming independent

CC distribution of microsatellites and MboI sites, the frequency of

CC (76)n >9 microsatellites in the bovine genome is estimated at >100,

CC (76)n >9 microsatellites in the bovine genome is estimated at >100,

CC on the sequence information for ca. 230 such bovine microsatellites

CC is summarised in the specification and indexed herein (see below).

CC the sequences upstream and downstream of the microsatellites sequence

CC were used to generate the required PCR primers for in vitro

amplification of the corresp. microsatellite (using the program

CC ompirky). The microsatellites may be used to identify individuals,

CC for parentage testing, and in the genetic mapping of economic trait

CC conjectures of in cattle, to allow selective breeding.

Sequence 62 BP; 22 A; 0 C; 31 G; 9 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9/c
033779 s
033779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amplification of the corresp. microsatellite (using the program). The microsatellites may be used to identify indiving for parentage testing, and in the genetic mapping of economic loci, or genes involved the determinism of economically import traits esp. in cattle, to allow selective breeding. See also Q33501-34437.

See also Q33501-34437.
                                                                                                                                                                             02-FEB-1993 (first entry)
Microsatellite sequence from clone AGLA29.
PCR; selection; primers; OPTIFRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                Q33594 standard; DNA; 63
Q33594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic mapping;
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA182. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                41 CTCTCTCTCTCTCTCTCTCTCACACACACACACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA;
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 0.1%;
Similarity 100.0%;
41; Conservative
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                             0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                             Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microsatellite (using the program es may be used to identify individuals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 41;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
0.00024;
0;
                                                                                                                                                                                                                                               0.0
Ed 0
                                                                                                                                                                                                                                             B 1; L
                cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cattle;
                                                                                                                                                                                                                                                              Length 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             program appling, and selective breeding

Table 7; Page 176; 517pp; English.

Table 7; Page 176; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by

CC The sequence is that of a bovine microsatellite sequence obtd. by

CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC one out of 50 clones cross-hybridised. Assuming independent

CC (15)n >9 microsatellites in the bovine genome is estimated at >100,

CC (000. The sequence information for ca. 230 such bovine microsatellites

CC is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence

were used to generate the required PCR primers for in vitro

compilfication of the corresp. microsatellite (using the program complification). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait

CC traits esp. in cattle, to allow selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PT Polymorphic bowlne DNA markers - used in genetic identification, properly properly and selective breeding Table 7; Page 167; 517pp; English.

CC The sequence is that of a bowlne microsatellite sequence obtd. by cc screening a library of bowlne mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. CC one out of 50 clones cross-hybridised. Assuming independent cd stribution of microsatellites and Mbol Sites, the frequency of CC (T6)n >9 microsatellites in the bowlne genome is estimated at >100, CC is summarised in the specification for ca. 230 such bowlne microsatellites completed to generate the required PCR primers for in vitro amplification of the corresp. microsatellite sequence complification of the corresp. microsatellite (using the program complification of in cattle, and in the genetic mapping of economic trait consists esp. in cattle, to allow selective breeding.

Sequence 63 BP; 22 A; 0 C; 32 G; 9 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-1993 (first entry)
Microsatellite sequence from clone AGLA8.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENM-) GENMARK.
Georges M, Massey
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                           Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q33618 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9213102-A.
06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q33618;
                                                                                                                                                                                                                                                                                                                                                                                (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                               US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          traits; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                      used in genetic identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
o. 0.00024;
o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 10
V19044/c
ID V19044
    ID ACC COS SOCIOTOR TO COS SOC
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                            29-JUN-1995.
21-DEC-1994; G02789.
21-DEC-1993; GB-026052.
(UYLE-) UNIV LEICESTER.
Armour J, Jeffreys AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24755 TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination

Example 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be present and an area of the process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN 1998.
15-JAN 1998.
09-JUL-1996; W0-U11478.
09-JUL-1996; WO-U11478.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                          Simple tandem repeat; STR;
                                                                                                                                                                                                                                                                                                                                    Q95218 standard; DNA; 85
Q95218;
                                                                                                                                                                                                           second
                                                                                                                                                                                                                                    characterisation; mapping;
                                                                                                                                                                                                                                                                                                         08-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be easily cloned and analysed. Sequence 40 BP; 7 A; 12 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of yeast artificial chromosomes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kouprina NY, Larionov VL, WPI; 98-110234/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces sp. WO9801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR; primer; amplification; Alu repeat sequence; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V19044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alu PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUI
                                                                                                                                                                                                                                                                                                                                                                                       ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                           95-240682/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .-1998 (first entry)
                                                                                                                                                                                                              part; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 100.0%;
40; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q33501-34437.
40 BP; 11
  simple tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
repeat
                                                                                                                                                                                                                                    corresponding to the 2nd part wg3b10; treatment; genetic; di linkage studies; analysis; all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB; Pred. No. 0.0
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05-MAR-1992.
27-AUG-1991; U06119.
27-AUG-1990; US-573570.
(UYRO) ROCKEFELLER UNIV.
(UYVE) UNIV OF VERMONT.
Heintz N, Heintz NH, Dailey
WPI; 92-096839/12.
                                                                                                                                Viral infection and cancer
Example 2: Page 42: 82pp; English.
Competition experiments using the DNAseI protection assay showed
that an oligonucleotide conty. 15 tandem ATT repeats was an
effective competitor for binding of the HeLa factor. This oligo was
used to prepare an oligonucleotide affinity column for purification
of RIP60 from Chinese hamster cells. The protein recognises and
binds to an (ATT)n motif in the dhfr gene ori. It can also bind to
the yeast ARS1 domain B. See Q22753 and Q24811.
Sequence 63 BP; 19 A; 5 C; 6 G; 33 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q24810
Q24810;
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   Q71808 standard;
Q71808;
30-MAR-1995 (fi
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oligonucleotide containing RIP60
Dihydrofolate reductase; stably b
DNA footprinting; (ATT)n binding
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ilarity 100.0%;
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New biocompatible medical devices and articles - using a lactic pri acid-glycolic acid polyester in which monomer units are rindividually and specifically determined by the principle of the specifically determined by the page 45; 67pp; English.

CC Encode polyesters given in 071801-02. This fragment was ligated into the Klenow blunted sequences given in 071808-09 which represent the 3' and 5' ends of the plasmid psport ib digested with Foki. This places this synthetic fragment under the control of the E. coli trpA initiator sequence was used to express the sequences given in 071801-02 in an E. coli cell free medium. The expressed complete the control of the polyesters derived from the a-maino acid analogues of an amino acid except pro. Of the three stop codons, URA, URA and UGA, one of these constrol trpA three stop codons, URA, URA and UGA, one of these codon, therefore the first lactate and glycolate are encoded by URA and URA codon. This is accomplished through the use of a specially modified complete the first lactate of the chain may be encoded by an CC encept modified to carry lactate instead of Met. Alternatively, a cresulting polymer is treated with cyanogen bromide to remove the Met. CC opon the first position of the polymer chain. The cresulting polymer is treated with cyanogen bromide to remove the Met. CC opon the sproduce in this manner may be used to produce sutures, cc staples, clips, drug delivery devices, pins and screws.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
01-JUL-1994.
31-DEC-1993; 112716.
31-DEC-1993; US-999520.
(USSU) US SURGICAL CORP.
Gruskin EA;
WPI; 94-272324/34.
Wew biocompatible medical devices and articles - understanding polyester in which monomer unit individually and specifically determined Example 2; Page 53; 67pp; English.
The sequences given in Q71814-16 represent fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1994.
31-DEC-1993; 112716.
31-DEC-1992; US-99953
(USSU) US SURGICAL (
                                                                                                                                                                                                                                                                                                                                                                             O/AB1;
30-MAR-1995 (first entry)
30-MAR-1995 (first entry)
Polyester coding sequence for insertion into pMAL-p2.
Polyester coding sequence for insertion acid analogue; cl
Synthetic gene; synthesis; polyester; a-amino acid analogue; cl
stop codon; stop signal; monomer unit; lactate; glycolate; stap
stop codon; stop signal; monomer unit; lactate; glycolate; stap
translation initiation; modified; Met-tRNAf; cyanogen bromide;
co-polymer; sutures; drug delivery device; screws; ds.
                                                                                                                                                                                                                                                                                                                                             Synthetic.
CA2112716-
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New biocompatible:
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Synthetic gene; synt
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gene; synthesis; polyester; a-amino acid analogue;
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Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New biocompatible medical devices and articles - using a lactic acid-glycolic acid polyester in which monomer units are individually and specifically determined

Example 1; Page 45; 67pp; English.

This sequence represents a fragment of the plasmid psporT Ic which contains the 5' fragment of the synthetic genes which encode polyesters, given in Q71801-02, under the control of the E. coli trpA transcription initiator and followed by FokI and HindIII restriction sites. A further fragment of the synthetic genes were ligated into psporT Ic to give plasmid psporT Id (see also Q71810-11), with the final fragment being inserted in a third round of ligation to give psporT Ie (see also Q71812).
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Sequence 81 BP; 47 A; 6 C; 4 G; 24 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stop codon; stop signal; monomer unit; lactate; glycolate; staples; translation initiation; modified; Met-tRNAf; cyanogen bromide; pins; co-polymer; sutures; drug delivery device; screws; ds.
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31-DEC-1992; US-999520.
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cc 13). The E. coli trpA initiator sequence was used to express the full cc length sequences given in Q71801-02 in an E. coli cell free medium. The expressed sequences represent synthetic genes which were used in the coli of polyesters derived from the a-maino acid analogues of an cc amino acid except pro. Of the three stop codons, UAA, UAG and UGA, one of these stop codons is reversed for the stop signal for the polyester. Cc units of the polyester. Lactate and glycolate are encoded by UAA and CC UAG, respectively. Initiation of translation always starts at an AUG codon, therefore the first lactate of the chain may be encoded by an CC Met. TRNAf modified to carry lactate instead of Met. alternatively, a met is incorporated in the first position of the polymer chain. The cc resulting polymer is treated with cyanogen bromide to remove the Met. Cc Co-polymers produced in this manner may be used to produce sutures, sequence 103 BP; 58 A; 7 C; 9 G; 29 T;
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                                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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	Sequence 183, App	Sequence 74, App.	Sequence 403, App	Sequence 400, App	Seguence 119, App	137	Sequence 397, App	Sequence 198, App	140	Sequence 358, App	Sequence 104, App	189	Sequence 77, App.	Sequence 322, App	Sequence 192, App	Sequence 180, App		Sequence 110, App	
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                               Sequence 430, Application US/08222177A Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%; Matches 54; Conservative 0;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UDABER: US 07/341,562
FILLING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sara, Charles S.
REGISTATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES 460
    TILE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
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STATE: Wiscons
                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (608) 831-2106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                              : 91 base pairs
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8000 Excelsior Drive, Suite 401
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                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                                                                                      0.2%;
LENGTH POLYMORPHISMS IN (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/222,177A
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                                                                                                                                                                                                                        Score 50;
Pred. No.
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                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                      DB 1; Length 91;
1.1e-07;
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Best Local S
Matches 50
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STATE: ML.
COUNTRY: USA
TO: 53717-1914
TEADABLE F
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                            APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Madison
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Sequence 65, Application US/08222177A Patent No. 5582979
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FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30.492
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 base pairs
TYPE: nucleic acid
                                                                      COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                   APPLICATION NUMBER: FILING DATE:
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8000 Excelsior Drive, Suite 401
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1
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100.0%; Pred. No. 1.:
1ve 0; Mismatches
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SAME

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US-08-222-177A-379; Sequence 379, Application US/08222177A; Patent No. 5582979;
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                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: SAIR, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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               STRANDEDNESS:
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                                               ENGTH:
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                             nucleic acid
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                                               50 base pairs
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8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber, James L.

VENTION: LENGTH POLYMORPHISMS IN

VENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                  (608) 831-2106
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linear
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100.0%; Pred. No
tive 0; Mismat
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; Sequence 44, Application US/08332766A
; Patent No. 5843647
; GENERAL INFORMATION:
                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-332-766A-44
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Best Local Similarity
"hes 41; Conserve
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                                                        Matches
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                         TELEPHONE: (202) 861-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JEFFREYS, APPLICANT: ARMOUR, J
40 CTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D. C.
                                                                                                                                                                                                                                                                                                                      NAME: BIRD, Donald J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                    NAME:
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                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                   85 base pairs
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                                                      Conservative
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                                                                    0.1%; Score 40;
100.0%; Pred. No.
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                                                      Mismatches
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                                                                                 DB 3;
                                                                    0.00018;
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RESULT 7 US-08-454-557C-57 ; Sequence 57, Application US/08454557C

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GENERAL INFORMATION:
APPLICANT: de la Monte,
APPLICANT: Wands, Jack |
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57, Appl. Patent No. 594863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,203
REFERENCE, DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIILE OF INVENTION: Neural Thread Protein Gene Expression and Detection
IIILE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection ITILE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08340426D
                                                                                                                                                                                                                           E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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1100 New York Avenue, Suite 600
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Wands, Jack R.
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14 - NOV - 1994
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100.0%; Pred. No.
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             US/08/340,426D
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0.0018;
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Best Local Similarity
Matches 37; Conserv
Query Match
Best Local Similarity
Matches 37; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
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                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzhelmer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/00 FILING DATE: 30-MAY-1995 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                  TOPOLOGY: bo
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                                                                                                                LENGTH: 60 base pairs TYPE: nucleic acid STRANDEDNESS: both
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1100 New York Avenue, Suite 600
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               0.1%; Score 37;
100.0%; Pred. No.
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                DB 4;
0.0018;
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0.0018;
                                 Length 60;
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   Indels
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21188 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCAC 21224

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RESULT 10
PCT-US95-17111A-57
; Sequence 57, Application PC/TUS9517111A
; GENERAL INFORMATION:
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PCT-US95-17111A-57
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                                                                                                                                                                           Sequence 69, Applicat Patent No. 5830670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                        21188 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCAC 21224
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                       TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/34
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                    APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                        ADDRESSEE:
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37; Conserv
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20005-3934
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Washington
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                1100 New York Avenue, Suite 600
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                                      Sterne, Kessler, Goldstein & Fox P.L.L.C
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100.0%; Pred. No.
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                                                                                                                                                      Suzanne
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0.0018;
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US-08-340-426D-69
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Best Local Similarity
                                       TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 69:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: |
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                               APPLICATION NUMBER: US/08/340,426D FILING DATE: 14-NOV-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609,38400
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
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CORRESPONDENCE ADDRESS:
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                   SEQUENCE CHARACTERISTICS:
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APPLICANT: Wands, Jack R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
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FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
LENGTH:
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   76 base pairs
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100.0%; Pred. No.
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0.0017;
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Best Local (
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Patent No. 5948888
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                                                                                     Sequence 69, Application PC/TUS9517111A
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                                                                     GENERAL INFORMATION:
                                                                                                                                                                                         21188 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCAC 21224
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release CURRENT APPLICATION DATA: APPLICATION NUMBER: US/OLF FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
             TITLE OF INVENTION:
                                        APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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Detection of Alzheimer's Di
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Pred. No.
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0.0017;
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0.0017;
               Disease
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STREET: 11
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STREET: 11
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REGISTRATION NUMBER:
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Query Match
Best Local Similarity
Matches 37; Conserv
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21188 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCAC 21224
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/3. FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                 ZIP: 20005-3934
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 20005-3934
                                       APPLICATION NUMBER: US/O FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                          COUNTRY: U.S.A.
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REFERENCE/DOCKET NUMBER: 0609.3840003

TELECOMMUNICATION INFORMATION:
TELEPHAN: (202) 371-2540

INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDESS: both
TOPOLOGY: both
US-08-454-557C-92

Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 35; Conservative 0; Mismatches 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0; Gaps 0

Qy 18907 GCCAGGATGGTCTCGATCTCCTGACCTCGTGATCC 18941
Db 9 GCCAGGATGGTCTCGATCTCCTGACCTCGTGATCC 43

Search completed: April 1, 2000, 04:07:52
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March 31, 2000, 13:42:06 ; Search time 8179.17 Seconds (without alignments)
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Copyright (c) 1993 - 2000 Compugen Ltd
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48: gb_est29: *
49: gb_est31: *
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51: gb_est31: *
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61: gb_est33: *
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64: gb_est33: *
65: em_est28: *
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67: em_est29: *
68: em_est30: *
69: gb_est44: *
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71: gb_est44: *
73: gb_est44: *
74: gb_est44: *
75: em_est33: *
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95: em_gss3: *
96: em_gss3: *
97: em_gss3: *
98: gb_gss3: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 1	Result
48	sult Query No. Score Match Length DB ID
48 0.2	% Query Match
102	Length
81	BB
102 81 B62983	ID
c 1 48 0.2 102 81 B62983 B62983 CIT-HSP-669	Description

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REFERENCE
AUTHORS
TITLE
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B62983/c
LOCUS
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ORGANISM
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CalTech Genome Research
California Institute of
Division of Biology, MS
     Division of Biology,
Tel: 626 796 7066
Fax: 626 395 4901
                                                                 Kim, U.-J., Adams, M.D. and Simon, M.I. Determination of clone end sequences
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Eutheria; Primates; Catarrhini; Hominida 1 (bases 1 to 102)
                                                                                                                                     B62983 102 bp D1
CIT-HSP-669F15.TP CIT-HSP
genomic survey sequence.
B62983
                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                              B62983.1
                                                                                                       Homo sapiens
ung@ash.tree.caltech.edu
                                                                                                                             GI:2636892
                                                                                                                                                                                                                       AA807640
N77004
AA873656
AI335049
HSMC09A06
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AA228795
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                    Lab
Technology
147-75, Pasadena,
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                                                                                                                                                    Homo
                                                                   sequences
                                                                                                                                                    sapiens
                                                                                         Hominidae;
                                                                   of human
                                                                                                                                                  GSS 21-JUN-1998 genomic clone 669F15,
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                      CA 91125,
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AA457423 aa86b02.r
D25845 HUMGS04217
A1475290 t181c11
                                                                   Bacterial Artificial
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A1864994 wk06c11.x
AA835411 ak72906.s
AA129957 zn86h04.r
AA669571 ac18d10.s
R67088 y130h05.s1
AU072757 AU072757
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R93021 yq1193.s1
H61099 yr51c12.r1
AA578401 n153c01.s
AA287473 n996b11.s
AA228795 nc14c07.s
AA807640 nx08b05.s
AA807640 nx08b05.s
AA80765 ce02g07.s
AA873656 ce02g07.s
AA873656 ce02g07.s
AI335049 ta44b01.x
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AQ28927 CTPBI-E1-
B80126 CIT HSP-204
AQ319270 RPCI11-98
A197331 WT3306.X
AQ27613 CITBI-E1-
R7073 Y14612.r1
AA601314 no15f06.s
AA082835 zn21912.s
AA082835 zn21912.s
AA809831 na40f11.s
AA809831 na40f11.s
R09732 Yf27a12.s
AR93021 Yq11903.s1
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AA053038 z171e12.s
AA835205 ak64h01.s
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B74378 CIT-HSP-202
AI088003 co24h05.x
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JOURNAL
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                                                                                                                                                                                                                                                   Eukaryota;
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Venter, J.C.
Use of BAC End Sequences for Sequence of BAC End Sequences for Sequence of Department of Eukaryotic Genomics The Institute for Genomic Research 19712 Medical Center Dr., Rockville, Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones are available from Research Genetics (info@resgen.com). BAend search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
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/db_xref="GDB:5491647"
/db_xref="taxon:9606"
/clone="669F15"
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI;
RPCII1 Human Male BAC Library"
                                                                      /db_xref="taxon:9606"
/clone="RPCI-11-4A12"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="sperm"
/note="Yector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                     /sex="Male"
                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                location/Qualifiers
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                                                                            TCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCTGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavic Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                    47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information http://grup.bio.unipd.it.
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HSPD19063 HM3 Homo sapiens cDNA clone s4000074G04, mRNA sequence.
F29274
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                                                                                                                                                                                                                                                            ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vect a 19 c 38 g 16 t
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000074G04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="HM3"
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100.0%; Pred. No.
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Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 25, 1995 this sequence version replaced gi:637795.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashUngton University School of Medicinep
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 74)

Marra,M., Hillier,L., Allen,M., Bowles,M., Districh,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 82)
                                                                                                               AI305512
AI305512.1
                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                         AI305512
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40m13 fwd.
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

5 c 17 g 6 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Organ: embryo: Vector: pBluescribe (modified);
Site_1: MluI; Site_2: Sall; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
Sall(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'. CDNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Knowles Solter mouse
/tissue_type="embryo"
/dev_stage="2-cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:790992"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="B6D2 F1/J"
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                                                                                                                 GI:3990403
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Pred. No.
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                                                                                                                                                                      sapiens cDNA clone
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0.00023;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: D.A.G.E. Consortium, LLNL
CDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington Clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                            Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiaspe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Le,M., Le,M., Le,M., Hultman,M., Kucaba,T., Parsons,J., Prange,C., Rifkin,L., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                      On May 18, 1995 this sequence version replaced Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                   Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                              and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 286 1800
1 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1996587"
/clone=lib="NCI_CGAP_Ov33"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="borderline ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="female"
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100.0%; Pr
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0.00045;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40M13 fwd, from Amersham.
                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos: Krizman,D., Kucaba,T., Laey,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU.NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA835205 101 bp
ak64h01.s1 Barstead |
IMAGE:1412689 3' sim
                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. Er from Amersham.

Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                              On Nov 29,
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/db_xref="taxon:9606"
/clone="IMAGE:1412689"
/clone_11b="Barstead pancreas HPLRB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:510094"
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/db_xref="GDB:3813427"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: Not
lst strand cDNA was primed with a Not I - oligo(dT) pr
                                                          /dev_stage="adult, 34 years"
/lab_host="DH10B"
                                                                                                 /sex="female"
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similar to contains Alu repetitive
element KER repetitive element; mRNA sequence
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Pred. No. 0.00043;
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source
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Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3137794.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI864984 90 bp mRNA EST 30-AUG-1999 wk06c11.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411540 3'similar to contains Alu repetitive element; mRNA sequence.
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
salr; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
a 29 c 27 g 21 t
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/db_xref="taxon:9606"
/clone="IMAGE:2411540"
/clone_lib="NCI_CGAP_Lyml2"
/tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                  /lab_host="DH10B"
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                                                                 Score 41; DB
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0.0041;
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AA129957
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                      AA129957 104 bp mRNA EST 27-NOV-1996 zn86h04.rl Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565111 5' similar to contains Alu repetitive element;, mRNA
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Location/Qualiflers
1. 97
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97)
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ilarity 100.0%;
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/db_xref="taxon:9606"
/clone="IMAGE:1413466"
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                                                                                       GI:1689679
                                                                                                                                                                                                                                                                                                                  Score 41; DB; Pred. No. 0.0 0; Mismatches
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 92.
Location/Qualifiers
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1 (bases 1 to 104)
1 (lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
1 Lennon,G., DuBuque,T., Favello,A., Gish,W.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
1 Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
1 Hawkins,B., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
1 Mardis,B., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
1 Robbits, Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
2 Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                           1 (bases 1 to 95),
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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WashU-NCI human EST Project
Unpublished (1997)
On Nov 6, 1997 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       ac18d10.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856819 3' similar to contains Alu repetitive element;, mRNA
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Fax: 314 286 1810
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             Homo sapiens
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/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="solit"
/lab_
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/db_xref="GDB:4594175"
/db_xref="taxon:9606"
/clone="IMAGE:565111"
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/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
                                                                                                                                                                                                                                                                                                                                                            GI:2631070
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  this sequence version replaced gi:932677
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                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
On Apr 5, 1995 this sequence version replaced Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 96)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Waterston, R., Williamson, A., Wohldmann, P. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4,0ml3 fvd. ET from Amersham.
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Fax: 314 286 1810
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     quality sequence stop: 65.
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/db_xref="taxon:9606"
/clone="IMAGE:856819"
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AU072757
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Matches 39
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JOURNAL
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                                                                                                                                                                                                                                                                                                                              University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU072757 73 bp mRNA EST 24-JUN-1999
AU072757 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSA765, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jun 5, 1998 this sequence version replaced gi:3188495. Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Developmental cDNA in Dictyostelium discoideum (1999) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum
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Conservative (
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                                                                                                       Similarity
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(bases 1 to 73)
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0 c 1 g 26 t
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/clone_lib="Soares placenta Nb2HP"
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0.02;
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0.0083;
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AU038446
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AU038446.1
EST.
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On Jan 14, 1998 this sequence version replaced g1:1798653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI262095 80 bp mRNA EST 13-NOV-1998 qz28c05.y1 NCI_CGAP_KId11 Homo sapiens cDNA clone IMAGE:2028200 5' similar to contains Alu repetitive element; contains TAR1 repetitive element; mRNA sequence.
AI262095 AI262095 AI262006
Dictyostelium discoideum Dictyostelium discoideum
                                                                                       AU038446 93 bp mRNA EST 29-MAR-1999
AU038446 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSH729, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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Location/Qualifiers
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library
                                                                                                                                                                                                                                                                                                                                                                                   Fatima Bonaldo. "
24 g
                                                                                                                                                                                                                                                                                                                                                                                                            (cloneIDs 1322376-1323911, 1456007-1456775,
1500552-1502855). Subtraction by Bento Soare
Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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Michael

29-MAR-1999

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E 1 (bases 1 to 93)

Norio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshido,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostelium developmental cDNA project; generation and analysis of expressed sequence tags from the first-finger stage of development

DNA Res. 5 (6), 335-340 (1998)

99156227

On Dec 5, 1997 this sequence version replaced gi:2662913.

Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba

1-2-10 Ton-codal Teukuba
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                                                                                                                                                                                                                                                                                                                               /organism="Dictyostelium discoideum"
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-6790.570 Million cell updates/sec
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         AR051487 60 bp DNA
Sequence 57 from patent US:
AR051487
 AR051487.1 GI:5974851
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M36131 Human alpha
M36132 Human alpha
M36132 Human alpha
L39139 Human alpha
L36836 Homo sapien
L36843 Homo sapien
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A68621 Sequence i
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M15365 Human low d
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L31083 Human STS U
X85061 B. taurus co
K02284 Human Doly
G37817 SAH Plasmo
AR051521 Sequence

K03556 Human low

29-SEP-1999

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BASE COUNT
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AF087511/c
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                                               CTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG 8783
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Homo sapiens clone ENaC+22 epithelial sodium channel alpha subunit
(SCNNIA) mRNA, alternatively spliced, partial sequence.
AF087511
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de la Monte, S. and War
Neural thread protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 66)
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ilarity 100.0%;
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<1. .>66
                                                                                                                                                                          /gene="SCNN1A"
20 c
                                                                                                                                                                                                            /note="alternatively spliced epithelial alpha subunit containing intronic Alu se
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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Location/Qualifiers
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14 c 15 g
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tive 0; Mismatches
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Kornreich, R., Bishop, D. F. and Desnick, R. J. Alpha galactosidase A gene rearrangements (Identification of short direct repeats at 1)
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l Similarity 100.0%; Pred. No.
46; Conservative 0; Mismatci
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J. Biol. Chem. 265, 9319-9326 (1990)
90264427
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de la Monte,S. and Wands,J
Neural thread protein gene
         Fabry disease;
Human DNA.
                                 M36132.1 GI:179542
                                           Human alpha-galactosidase M36132
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/db_xref="taxon:9606"
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                      breakpoint junction; glycosphingolipid catabolism.
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                                                                                                                                                                                                                                                               Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: AGTTCGAGACCAGCCTGGC
Primer B: AGGTGGCAGAAAATCGCATC
End to Label: Primer A
PCR Profile:
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L39139 L18336
L39139.1 GI:642101
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J. Biol. Chem. 265, 9319-9326 (1990)
90264427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kornreich, R., Bishop, D.F. and Desnick, R.J. Alpha-galactosidase A gene rearrangements causing Fabry disease: Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted by: Utah Center for Human Genome Research University
                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen.H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 69)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White, R.
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10 sec. 62 C 10 sec. 72 C 20 sec.
18 C 10 sec. 72 C 20 sec. Mg++: 1.50
1. Acrylamide 7%, Formamide 32%, Urea 34%
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                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19"
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Best Local S
Matches 43
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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 0.1%; Score 43; DB Similarity 100.0%; Pred. No. 3: 43; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens 4000 year 136836
                                                                                                enzymatic amplification Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ancient DNA: extraction, characterization, molecular cloning, enzymatic amplification
Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                       Homo sapiens (individual_isolate 4000 year Nekht-ankh) liver DNA.
                                                                                                                                                                                                                                                                       Alu repeat
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                                                                                                                                 Ancient DNA: extraction, characterization, molecular cloning,
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/isolate="4000 year old r.
/db_xref="taxon:9606"
/tissue_type="liver"
<1...>65
/organism="Homo sapiens"
/isolate="4000 year old
/db_xref="taxon:9606"
                                                                 Location/Qualifiers
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17 c 21 c
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                 remains
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Nekht-ankh Alu repeat
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/tissue_type="liver"

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RESULT 9
A68621/c
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HUMALCE221/c
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Best Local Similarity
Matches 43; Conserv
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Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                TITLE
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                                                                                                                                 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences

J. Mol. Biol. (1992) In press

J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A68621 40 bp DNA
Sequence 1 from Patent WO9801573.
A68621
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Human carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unclassified.

1 (bases 1 to 40)

1 (bases 1 to 40)

Resnick,M.A., Larionov,V.L., Kouprina,N.Y. and Perkins,

TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING

Patent: WO 9801573-A 15-JAN-1998;

US HEALTH (US)
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/rpt_family="Alu"
18 c 23
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/db_xref="taxon:32644"
12 c 13 g
                                                          /db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
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               /tissue_type="carcinoma"
27 c 33 g 1
                                            /sex="male"
                                                                                                      organism="Homo sapiens"
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FEATURES
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HUMBRKFAC
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AR051522
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Query Match
Best Local S
Matches 37
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Best Local Similarity
Matches 39; Conserv
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Local Similarity 100.0%; Pred. No. 1e-08;
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90264427
 . Similarity 37; Conserv
                                                                                                                                                                                                            1 (bases 1 to 80)

Kornreich, R., Bishop, D.F. and Desnick, R.J.

Alpha-galactosidase A gene rearrangements causing Fabry disease:

Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             HUMBRKFAC 80 bp DNA PRI Human alpha-galactosidase breakpoint region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: US 5830670-A 92 03-NOV-1998;
Location/Qualifiers
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de la Monte, S. and Wands, J.R.
Neural thread protein gene ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR051522 85 bp DNA
Sequence 92 from patent US 5830670.
AR051522
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                                                                                                                                                                                             Alu-rich
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   Conservative
                                                                                                                                                                                Chem. 265, 9319-9326 (1990)
                                                                                                                                                                                                gene
                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
28 c 17 g 1
                                                                                                                                      Location/Qualifiers
1. .80
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27 c 25 g
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0.1%; Score 37; DB
100.0%; Pred. No. 3.
tive 0; Mismatches
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DB 9; Length 80;
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GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC

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   TGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1
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1 (bases 1 to 90)

Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.

Duplication of seven exons in LDL receptor gene caused by Alu-Alu recombination in a subject with familial hypercholesterolemia Cell 48 (5), 827-835 (1987)
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17 a 30 c 24 g 19 t
Chromosome 19p13.2-p13.1.
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Alu repeat; low density lipoprotein receptor-1;
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37; Conservative
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                                                       0.1%; Score 36; DB 5; I larity 100.0%; Pred. No. 1.1e-06; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/map="19p13.3"
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llarity 100.0%; Pred. No. 1.1e-06;
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Page 6

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   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Microsatellite seq

(dC-dA)n. (dG-dT)n

Microsatellite seq

Sequence of a micr

Repeat sequence fr

Microsatellite seq

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65743 standard; DNA; 40

ВP

6

Homo sapiens. US5582979-A.

21-APR-1989; 341562

765743; 197 (first entry)
17-JUN-1997 (first entry)
17-JUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd42.
Repeat sequence; genetic marker; primer; amplification; Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

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simi	4 standard; 4;-1998 (fir 1-1998 (fir CR primer; ampl lar yeast ar etic. 1573-A1. 11573-A1. 11-1996; WO-U 1-1996; WO-U 1-19	
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o;	IN BP. Lion; Alu repeat sequence; lal chromosome; YAC; ss. Lion; Alu repeat sequence; ss. Lion; Alu repeat sequence; ss. Lion; Alu repeat sequence MA; resnick MA; retificial chromosomes - by the comprising yeast centricial cacid for recombination pp; English. Liourepeat sequence, which i sequence for the PCR prime lu repeat sequence, which i cricular yeast artificial pecific nucleic acids from introducing the vector(s) pidly isolate human DNA when the comprise the vector(s) pidly isolate human DNA when the comprise the methods largualysed. A; 12 C; 13 G; 8	T65744 T65778 T65777 T65777 T65717 T65711 034068 033828 03382 033882 033953 033953
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re 40; DB ed. No. 0. Mismatches	repeat sequence; voosome; YAC; ss. SERVICES. ns EL, Resnick MA; chromosomes - by in rising yeast centron for recombination ish. for the PCR primer sequence, which is loed in the invention r yeast in the invention r yeast in the invention ing the wector(s) in late human DNA where g the methods large C; 13 G; 8 T	744 7748 7772 7711 711 711 711 819 819 828 828 828 829 953 974 906
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DR WPI; 97-042299/04.

DR WPI; 97-042299/04.

DR Detection of polymorphic genetic markers of the form protection of polymorphic genetic acid mols. as primers (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Primers (dC-dA)n - (dS-dT)n - (dS-
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21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754551.
04 APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
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05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
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Repeat sequence from polymorphic marker clone Mfd7.

Repeat sequence from polymorphic marker; primer; amplification;

Polymorphism; repeat sequence; genetic marker; primer; amplification;

POR; polymerase chain reaction; paternity; maternity; human; pedigree;

POR; polymerase chain reaction; paternity; maternity; human; pedigree;

linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                                                                                                                                                                                                                                                                                                                                            PT Polymorphic bowlne DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
PS Table 7; Page 379; 517pp; English.

CC The sequence is that of a bowlne microsatellite sequence obtd.
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bowlne genome is estimated at >100,
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC optiprimy). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economicatily important
CC see also Q33501-34437.
SQ Sequence 49 BP; 7 A; 0 C; 17 G; 25 T;
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06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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         (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                      genetic mapping;
Bos taurus.
                                                                                                                  02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA272.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of a microsatellite from clone TGLA68. PCR; selection; primers; OPTIPRIM; breeding; cattle; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey
WPI; 92-284684/34.
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15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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                                                                                                                                                                                  Q33870 standard; DNA; 54 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENM-) GENMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
36; Conser
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.1%;
llarity 100.0%;
Conservative (
  bowine DNA
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                0.1%;
  markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                 Score :
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
 used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 36;
No.
                                                                                                                                                                                                                                                                                                             36;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
2.6;
                                                                                                                                                                                                                                                                                                                  2 DB
genetic identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٠
                                                                                                                                                                                                                                                                          29034
                                                                                                                                                                                                                                                   36
                                                                                                                                                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                                                                             1:
                                                                                                                                 cattle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 46;
                                                                                                                                                                                                                                                                                                                            Length 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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T65737; T67737; AC T65737; Standard; DNA; 45 AC T65737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PT gene mapping, and selective breeding
Table 7; Page 277; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC one out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (76)n >9 microsatellites in the bovine genome is estimated at >100,
CC occurrence information for ca. 230 such bovine microsatellites
CC occurrence information and indexed herein (see below).
CC is summarised in the specification and indexed herein (see below).
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellites for primers for in vitro
CC maplification of the microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC see also 033501-34437.
SO Sequence 54 BP; 1 A; 0 C; 26 G; 27 T;
                                                                                                                                                              Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-1992.
24-JAN-1991; NL-000132.
25-JAN-1991; NL-000132.
(INCE-) INCENY BV
Ultterlinden AG, Vijg J;
WPI; 92-284683/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 6; 31pp; English.

Primer PDJ33 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can be used to detect genetic variation.

See Q27389-Q27404 and Q33141-Q33144.

Sequence 35 BP; 8 A; 10 C; 11 G; 6 T;
                                                                                               Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic. WO9213101-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q27391 standard; DNA; 35 B
Q27391;
27-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inter-Alu specific Polymerase chain re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                            ch 0.1%; S
l Similarity 100.0%;
35; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 0.1%;
1 Similarity 100.0%;
36; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lc primer PDJ33.
reaction; PCR; repetitive element;
                                                                                                                                                              Score 35; DB; Pred. No. 4.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                             DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
2.5;
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                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 54;
                                                                                                                                                                                             Length 35
                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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RESULT
Q34053/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pr decedion of polymorphic genetic markers of the form (dc-dA)n(dg-dT)n - using novel nucleic acid mols. as primers blsclosure; Column 9-10; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences (dc-dA)n.(dg-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, thuman genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dg-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat concerns the form the marker clone Mdf36 which contains the repeat sequence is from the marker clone Mdf36 which contains the repeat concerns and the formula: (AC)15AT(AC)5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                          06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754331.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding gene mapping, and selective breeding Table 7; Page 352; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence
                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA438. FCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss. Bos taurus.
WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-FEB-1993 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q34053 standard; DNA; 62 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 97-042299/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd36.
Polymorphism; repeat sequence; genetic marker; primer; amplificati
PCR; polymerase chain reaction; paternity; maternity; human; pedig
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MARS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
PCR primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                         cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pedigree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT
T66109,
ID T6
AC T6
DT 18
DE (0
KW P6
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                                                                                                                                                                                                                                  跊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene mapping, and selective breeding
Table 7; Page 225; 517pp; English.
The Sequence is that of a bovine microsatellite sequence obtd. by
Combined the sequence is that of a bovine microsatellite sequence obtd. by
Combined the sequence of bovine MboI DNA fragments of between
Combined the sequence of bovine MboI DNA fragments of between
Combined the sequence of bovine MboI DNA fragments of between
Combined the sequence of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding.

See also 033501-34437.

Sequence 62 BP; 21 A; 0 C; 10 G; 31 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                            See also
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsatellite sequence from clone TGLA153. PCR; selection; primers; OPTIPRIM; breeding; cattle; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q33737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q33737 standard; DNA;
18-JUN-1997 (first entry) (dC-dA)n.(dG-dT)n polymorphic Polymorphism; repeat sequence; PCR; polymerase chain reaction
                                                                                           T66109 standard; DNA; T66109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L5-JAN-1992;
L5-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                              10
                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                                                                                                                                                                                                                                       parentage testing, and in the genetic mapping of economic trait, or genes involved the determinism of economically important tesp. in cattle, to allow selective breeding.

also Q33501-34437.

puence 39 BP; 2 A; 0 C; 17 G; 20 T;
                                                                                                                                                                                                                                                                             TATGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATATATATATATATATATATATATATACA
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                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                    0.1%; Sur
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.1%;
lymorphic double perfect repeat sequence.
sequence; genetic marker; primer; amplification;
reaction; paternity; maternity; human; pedigree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                   47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                           Score 34; DB Pred. No. 7.9
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in
                                                                                                                                                                                                                                                                                                                                                     7.9
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7.
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                                                                                                                                                                                                                                                                             29034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic identification,
                                                                                                                                                                                                                                                                                                                                                   .9
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                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parentage;
                                                                                                                                                                                                                                                                                                                             0
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  pedigree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                             0
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RESULT
Q34056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the isolation of polymorphic repeat sequences con having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic contexts, especially for use in e.g paternity or maternity testing, commercial analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis.

CC commercial animal or plant breeding or pedigree analysis.

CC the repeats, when analysed, fall into 4 categories:

CC liperfect repeats which are alternating tandem CA repeats with no context separated by no more than 3 consecutive non-repeat bases;

CC jimperfect repeats which are defined as 2 or more runs of uninterrupted compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases;

CC interruptions and without adjacent repeats from a run of at least compound perfect repeats which are uninterrupted runs of the perfect compound repeats which are uninterrupted of a sequence other than conformat least 10 uninterrupted mononuclectides; and compound repeats except that the runs of CA are interrupted.

CC This sequence with structure: A(CA)ISTACG(CA)6, would be scored as 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29000 GTATGTGTGTGTGTGTGTGTGTGTGTGTGT
polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding Table 7; Page 353; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).
                                                                                                                                                                                                                                                                                                                                                                                                          Q34056
Q34056;
                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA44. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as Disclosure; Column 349-350; 186pp; English.
                                                                                                                                                                                              Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linkage analysis;
                                                                                                                                                                                                                                                                                    WO9213102-A.
06-AUG-1992.
                                                                                                                                                                                                                                 (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MARS-) MARSHFIELD
                                                                                                                                                                                                                                                 .5-JAN-1992; U00340.
.5-JAN-1991; US-642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
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32979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           perfect repeat 47 BP; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.1%;
nilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 22 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,08;
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Pred. No. 7.4
0; Mismatches
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7.4;
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                                                                                                                                                                                                                                                                                                                                                       cattle; parentage
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                                                                                                                                                                                                                                                                                                       gene mapping, and selective breeding

Table 7; Page 304; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine microsatellite sequence obtd. by

cone out of 50 clones cross-hybridised. Assuming independent

distribution of microsatellites and MboI sites, the frequency of

(T6)n >9 microsatellites in the bovine genome is estimated at >100,

000. The sequence information for ca. 230 such bovine microsatellites

is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence

were used to generate the required PCR primers for in vitro

applification of the corresp. microsatellite (using the program

copTIPRIM). The microsatellites may be used to identify individuals,

for parentage testing, and in the genetic mapping of economic trait

loci, or genes involved the determinism of economically important

contraits esp. in cartile. To allow selective breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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                                                                                                                                         29001 TATGTGTGTGTGTGTGTGTGTGTGTGTGTG 29034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIFRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also Q35501-34437.
                                T26728 standard; cDNA to mRNA; T26728;
                                                                                                                                                                                                                                                                 traits esp. in cattle, to allow selective breeding. See also Q33501-34437. Sequence 79 BP; 16 A; 0 C; 24 G; 39 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM; WPI; 92-284684/34.
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Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q33936 standard; DNA; 79 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-1993 (first entry)
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                 22-OCT-1996 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selection; primers;
                                                                                                                            TATGTGTGTGTGTGTGTGTGTGTGTGTGTG
 gene signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                     Similarity 100
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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100.08; Pr
                                                                                                                                                                                                  0.1%;
 HUMGS08978
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OPTIPRIM; breeding;
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Pred. No.
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Pred.
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No.
                                                                                                                           63
                                                                                                                                                                                                     DB 1
6.2;
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Claim 1; Page 2158; 2245pp; Japanese.

Claim 1; Page 2158; 2245pp; Japanese.

Claim 2; Page 2158; 2245pp; Japanese.

Claim 2; Page 2158; 2245pp; Japanese.

Claim 2; Page 2158; 2245pp; Japanese.

Claim 3; Page 2158; Page 2158;
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Best Local S
Matches 34
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W09514772-A1.

01-JUN-1995.

11-NOV-1994; J01916.

12-NOV-1993; JP-355504.
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Microsatellite sequence from clone TGLA261.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
Bos taurus.
                                    gene mapping, and selective breeding
Table 7; Page 271; 517pp; English.
Table 7; Page 271; 517pp; English.
The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between
250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
One out of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and MboI sites, the frequency of
(T6)n >9 microsatellites in the bovine genome is estimated at >100,
000. The sequence information for ca. 30 such bovine microsatellite
is summarised in the specification and indexed herein (see below).
The sequences upstream and downstream of the microsatellite sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsubara K, Okul
WPI; 95-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
    The sequences upstream were used to generate t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q33855
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Pred. No.
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5.7;
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          밁
                                                                                                                                                                                                                                                                                                  PT gene mapping, and selective breeding
PT Table 7; Page 271; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC Screening a library of bovine MboI DNA fragments of between
CC One out of 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC One out of 50 clones cross-hybridised. Assuming independent
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC out of the sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economicatly important
CC see also Q33501-34437.
CC Sequence 44 BP; 22 A; 0 C; 0 G; 22 T;
                                                                                                                                           Query Match
Best Local Similarity
Matches 33; Conserv
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Matches 33; Conservative (
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15-JAN-1992; U003
15-JAN-1991; US-6
(GENM-) GENMARK.
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See also 033501-34437.

Sequence 44 BP; 22 A; 0 C; 0 G; 22 T;
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Microsatellite sequence from clone TGLA261.
Microsatellite sequence from clone TGLA261.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
WPI; 92-284684/34.
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ilarity 100.0%;
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Search completed: April Job time: 291698 sec

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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/1/1na/5D_COMB.seq:*
/cgn2_6/ptodata/1/1na/6_COMB.seq:*
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US-08-454-557C-92

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US-08-454-557C-92

US-08-450-673C-92

US-08-222-177A-71

US-08-222-177A-71

US-08-222-177A-157

US-08-222-177A-159

US-08-222-177A-159

US-08-252-177A-149

US-08-450-673C-91

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Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence
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ALIGNMENTS

RESULT 1 US-08-454-557C-57 ; Sequence 57, Application US/08454557C ; Patent No. 5830670 ; US-08-454-557C-57 STREET: 1100 New York Avenue, Suite 600 STRATE: D.C. COUNTRY: Washington STATE: D.S.A. ZIP: 20005-3934 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/454,557C FILING DATE: 30-MAY-1995 CLASSIFICATION: 514 ATTORNEY_AGENT INFORMATION: NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609.384000: TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600 GENERAL INFORMATION: APPLICANT: We la Monte, Suzanne APPLICANT: Wands, Jack R. TITLE OF INVENTION: Neural Thread Protein Gene TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121 TELEPHONE: (202) 371-2540 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: LENGTH: 60 base pairs TYPE: nucleic acid STRANDEDNESS: both ADDRESSEE: 3: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600 both 0609.3840003 Expression and Detection

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Query Match Best Local S Matches

Local

ch 0.2%; 1 Similarity 100.0%; 46; Conservative

Score 46; pred. No.

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Mismatches

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Best Local Similarity
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APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Meural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            TILE OF INVENTION: Neural Thread Protein Gene Expression and Detection ITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/340,426D FILING DATE: 14-NOV-1994 CLASSIFICATION: 435
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                                                                COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                                                                E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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Sequence 57, Application PC/TUS9517111A
GENERAL INFORMATION:
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Best Local Similarity
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SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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APPLICANT: Wands, Jack |
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                                                                                                                               NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                 ELEPHONE:
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: 60 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
                                                             w: (202) 371-2600
(202) 371-257
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Detection of Alzheimer's Disease
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n Release #1.0, Version #1.25
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Pred. No.
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RESULT 5
US-08-454-557C-69
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                                                                                      Sequence 69, Application US/08340426D Patent No. 5948634 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                       APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 371-2600
                           TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
CORRESPONDENCE ADDRESS
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REFERENCE/DOCKET NUMBER: 0609.3840003
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46; Conserv
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Wands, Jack R.
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Pred. No.
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Pred. No.
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             REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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US-08-450-673C-69
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                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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MEDIUM TYPE: Floppy disk
                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
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STREET: 1100 New
CITY: Washington
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STRANDEDNESS: both
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                         NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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Ludwig, Steven R.
Ludwig, Steven R.
AGENT AND AGENT A
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1100 New York Avenue, Suite 600
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ork Avenue, Suite 600
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0609.3840004
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Pred. No.
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RESULT 9
US-08-454-557C-92
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Matches
                                                                                                                                  Query Match
Best Local Similarity
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                                                                          25363 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGC 25408
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                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R. 203
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NITLE OF INVENTION: Neural Thread Protein Gene Expression OF INVENTION: Detection of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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20005-3934
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100.0%;
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100.0%; Pred. No.
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Pred. No.
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RESULT 10
US-08-340-426D-92
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US-08-454-557C-92
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APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
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INFORMATION FOR SEQ ID NO:
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                               COMPUTER READABLE FORM:
MEDITM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
              CURRENT APPLICATION DATA
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
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                                                                                                                                      COUNTRY: U.S.A.
ZIP: 20005-3934
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L00.0%; Pred. No. 0.00086;
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US/08/340,426D
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US-08-450-673C-92
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       Query Match 0.1%; Score 39; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 39; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNAY DESCRIPTION:
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
                                                                                                                                                                                                                              TELEPHONE: (202) 371-2600
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
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                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: both
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39; Conservative
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20005-3934
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                                                                                                                                                                                                              (202) 371-2600
(202) 371-2540
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o. 0.00086;
0;
DB 4; Lc., 0.00086; 0;
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RESULT 13
US-08-222-177A-175/c
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; Sequence 92, Application PC/TUS9517111A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-17111A-92
                                                                                                                                                                                           Sequence 175, Application US/08222177A Patent No. 5582979
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                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                      GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUEN
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 371-25 TELEFAX: (202) 371-25 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/340,42

FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: LUCWIG; Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: Detection of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 New 1
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20005-3934
                                    STREET:
                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                               9 GCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCC 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                  Madison
Wisconsin
                                  E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        both
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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US-08-222-177A-71/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
RECISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                          COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NOMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: mfd42rs
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 TGTATGTGTGTGTGTGTGTGTGTGTGTGTGTG
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                                                                                                                                                                                                                                                                                STATE: Wisconsin
                                                                                                                                                                                                                                                                                                     CITY: Madison
                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
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                                       US 07/341,562
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Query Match
Best Local Similarity
Matches 36; Conserv

0.1%; Score 36; DB ilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches

DB 2;

Length 54;

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RESULT 15
US-08-469-802B-27/c
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                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 612-305-1225 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0: FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (608) 831-2106
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                                                                             LENGTH: 54 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                      linear
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Minimum DB Maximum DB

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Post-processing: Listing first 45 summaries
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Perfect score:
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      US-08-852-495C-1_COPY_206000_235033
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1 AGTTGTAATAGGTAGAACAA.....TGTC
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em_est9:*
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zn21g12.s1 Stratagene neuroepithelium
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Fax: 314 286 1810
Email: est@watson.v
                        9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(Pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f
Research Genet cs (lnfo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.h
Seg_primer: T7
                                                                                                                                                                                        Contact: Shaying Zhao, William Nie:
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Sep 12, 1996 this sequence version Contact: Wilson RK Washington University School of Medici 4444 Forest Park Parkway, Box 8501, St Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                AQ535244 103 bp DNA RPCI-11-317H22.TV RPCI-11 Homo RPCI-11-317H22, genomic survey AQ535244 1 GI:4846934
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59; Conserv
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40M13 fwd. from Amersham.
                                                                                                                                                                                                                                                         Map Building
Unpublished (1997)
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Use of BAC End Sequences
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/db_xref="GDB:3926650"
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/clone="IMAGE:548134"
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/dev_stage="Ntera-2/RA+MI neuroepithelial cells"
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AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Inpublished (1997)
On May 1, 1997 this sequence version replaced
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 72)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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                                                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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/organism="Homo sapiens"
/db_xref="GDB:7621533"
/db_xref="taxon:9606"
/clone="RPCI-11-317H22"
/clone_ib="RPCI-11"
                                                                   /note="organ: ovary: Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
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RPCII1 Human Male BAC Library"
27 c 27 g 18 t
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/db_xref="taxon:9606"
/clone="IMAGE:2219558"
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/lab_host="DH10B"
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B48914
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CIT-HSP-669F15.TP CIT-HSP Homo sapiens genomic clone 669F15,
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Class: BAC ends.
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California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA
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Fax: 626 395 4901
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Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 103)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jone
                                                                                                                                                      On Apr 7, 1998 this sequence Contact: Valle G.
                                                                                                                                                                                                                    Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavic: Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization sequences. 6 (1), 35-42 (1996)
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48; Conserv
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Seq primer: SP6
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Clones are derived from the human BAC library RPCI-11. For BA
Clones availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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Use of BAC End Sequences for Sequence-Ready Map Building
                                  Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information http://grup.bio.unipd.it.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8621 TCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCTGCCACC 8667
                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Chissoe,S., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Mardis,E., Moore,B., Mortis,M., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
T94466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 614
High quality sequence stops: 70 Source: IMAGE Consortium, clone is available royalty-free through LLNL; contact the Consortium (info@dimage.llnl.gov) for further information.
Insert Length: 614 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ye35b02.rl Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119691 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                            quality sequence stop: 70.
Location/Qualifiers
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llarity 100.0%; F
Conservative 0;
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/note="Yector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer
(5'-biotin-AACCCGGCTCGAGCGGCCGCTTTTTTTTTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector."

18 a 19 c 38 g 16 t
/organism="Homo sapien.
/db_xref="GDB:487980"
/db_xref="taxon:9606"
/clone="IMAGE:119691"
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/db_xref="taxon:9606"
/clone="s4000074G04"
/clone_lib="HM3"
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Pred. No.
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0.0001;
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24-MAR-1995

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             17445 GGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCT 17488
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GGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCT
                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N84707 70 bp mRNA
J0579F Human fetal heart, Lambda ZAP
Clone J0579 5' similar to REPETITIVE
                                                                                                                                                                                                                                                                                                                                           Fax: 4169785650
Email: liewcc@utcc.utoronto.ca
Seg primer: GAAATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                          Banting Institute, 100 College St., Tel: 4169788758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 70)
                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Laboratory Medicine and Pathobiology University of Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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47; Conservative
                                                                     Similarity
                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

18 c 15 g 13 t
                                                                                                                                                                                                                                                                         /clone="J0579"
                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Stratagene lung (#937210)"
/sex="male"
                                                                                                                                                                                                                                                       clone_lib="Human fetal heart, Lambda ZAP Express"
                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                  0.2%;
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Pred. No.
                                                                  Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1996)
                                                      Mismatches
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                                                                DB 25;
0.0011;
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9.4e-05;
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EXPRESS HOMO SAPIENS CDNA
ELEMENT ALU, mRNA SECULO
                                                                               Length 70;
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                                                                                                                                                                                                                                                                                                                                                                                             19018 GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCC 19061
                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                        Okubo, K., Fukushima, A., Yoshii, J.,
                                                                                 Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                          Homo sapiens
                                                                                                                                                                     EST
                                                                                                                                                                                                                                                 HUMGS01971 Human promyelocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information http://grup.bio.unipd.it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRIBI Biotechnology Centre University of Padua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96276048
On Jun 5, 1998 this sequence version replaced gi:3188834
Contact: Valle G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSPD10834 HM3 Homo sapiens
Yoshinari,H., Arimoto,J. and Matsubara,K.

Gene expression of human promyelocytic cell line HL60 before and
                                                                                                                                                                                       D20989.1
                                                              (bases 1 to 87)
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                                                                                                                                                                                                                               sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pectoral muscle (after mastectomy)"
/note="vector: pcDNAII (Invitrogen); Site_1: BGXXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer
(5'-biotin-AACCCGGCTCGAGCGGCCGCTTTTTTTTTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector."

18 a 21 c 19 g 22 t
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/db_xref="taxon:9606"
/clone="s4000013A06"
/clone_lib="HM3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.2%;
                                                                                                                                                                                                                                                                        87 bp
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                 Homo sapiens cDNA clone mp0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 50;
. 0.00098;
                                        Niiyama, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA835205 101 bp mRNA EST 23-FEB-1998 ak64h01.sl Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412689 3' similar to contains Alu repetitive element; contains element KER repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On Nov 29, 1993 this sequence version replaced g1:636226
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101)
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                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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              /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
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                                                                                                                       /sex="
                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1412689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type
promyelocyte. "
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/db_xref="taxon:9606"
/clone="mp0383"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
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                                                                                                                                        /clone_lib="Barstead pancreas
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8577 ATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATT 8619
                                            8577 ATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCA 8617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On May 18, 1998 this sequence version replaced gi:3137794. Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 90)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2411540"
/clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, foili
cell"
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136 c 27 g 24 t
                                                                                                                                                                                                                                /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Notl; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

2 7 9 21 t
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On Sep 12, 1996 this sequence version replaced gi:1407381.
Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 134 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                AA226656 102 bp mRNA EST 21-AUG-1997 nc19f09.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008617 similar to contains Alu repetitive element;, mRNA sequence.
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 102)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1309483.
Contact: Robert Strausberg, Ph.D.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="IMAGE:867791"
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Unpublished (1998)
Other_GSSs: CIT-HSP-2163G1.TF
Other_GSSs: CIT-HSP-2163G1.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
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cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                               Simon,M. and Venter,J.C.
Use of a random BAC End Sequence
Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linhe. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
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Location/Qualifiers
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